Access DB# 32250

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: Joe Zhou Examiner #: 78282 Date: 1/3/01

Art Unit: 1631 Phone Number 30 605-1158 Serial Number: 09/641081

Mail Box and Bldg/Room Location: [redacted] Results Format Preferred (circle): PAPER DISK E-MAIL

(2001)

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

***For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.**

BEST AVAILABLE COPY

****

STAFF USE ONLY	Type of Search		Vendors and cost where applicable	
Searcher: [illegible]	NA Sequence (#)		STN	✓
Searcher Phone #: 4498	AA Sequence (#)		Dialog	
Searcher Location:	Structure (#)		Questel/Orbit	
Date Searcher Picked Up: 1/25	Bibliographic	✓	Dr.Link	
Date Completed: 1/26	Litigation	✓	Lexis/Nexis	
Searcher Prep & Review Time:	Fulltext		Sequence Systems	
Clerical Prep Time: 30	Patent Family		WWW/Internet	
Online Time: + 120	Other		Other (specify)	

PTO-1590 (1-2000)

L6 ANSWER 1 OF 1 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:398753 BIOSIS
DOCUMENT NUMBER: PREV200000398753
TITLE: Use of high density oligonucleotide arrays to assist in **transcriptional annotation** of the E. coli genome.
AUTHOR(S): Rosenow, C. I. (1); Saxena, R. Mukherjee (1); Gingeras, T. (1)
CORPORATE SOURCE: (1) Affymetrix, Santa Clara, CA USA
SOURCE: Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 446. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology Los Angeles, California, USA May 21-25, 2000 American Society for Microbiology
. ISSN: 1060-2011.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
CONCEPT CODE: Physiology and Biochemistry of Bacteria *31000
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Genetics of Bacteria and Viruses *31500
Virology - Bacteriophage *33504
BIOSYSTEMATIC CODE: Bacterial Viruses - General 02700
INDEX TERMS: Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
INDEX TERMS: Chemicals & Biochemicals
RNA
INDEX TERMS: Methods & Equipment
high density oligonucleotide arrays: analytical method, genetic method
INDEX TERMS: Miscellaneous Descriptors
Escherichia coli genome: **transcriptional annotation**; bacterial genetics; Meeting Abstract; Meeting Poster
ORGANISM: Super Taxa
Bacterial Viruses: Viruses, Microorganisms; Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms
ORGANISM: Organism Name
Escherichia coli (Enterobacteriaceae); bacteriophage (Bacterial Viruses)
ORGANISM: Organism Superterms
Bacteria; Bacterial Viruses; Eubacteria; Microorganisms; Viruses

Trying 3106016892...Open

Welcome to STN International! Enter x:x
LOGINID:SSSPTA1635SXZ
PASSWORD:
TERMINAL (ENTER 1, 2, 3, OR ?):2

* * * * * * * * * * Welcome to STN International * * * * * * * * * *

NEWS 1		Web Page URLs for STN Seminar Schedule - N. America
NEWS 2	Dec 17	The CA Lexicon available in the CAPLUS and CA files
NEWS 3	Feb 06	Engineering Information Encompass files have new names
NEWS 4	Feb 16	TOXLINE no longer being updated
NEWS 5	Apr 23	Search Derwent WPINDEX by chemical structure
NEWS 6	Apr 23	PRE-1967 REFERENCES NOW SEARCHABLE IN CAPLUS AND CA
NEWS 7	May 07	DGENE Reload
NEWS 8	Jun 20	Published patent applications (A1) are now in USPATFULL
NEWS 9	JUL 13	New SDI alert frequency now available in Derwent's DWPI and DPCI
NEWS 10	Aug 23	In-process records and more frequent updates now in MEDLINE
NEWS 11	Aug 23	PAGE IMAGES FOR 1947-1966 RECORDS IN CAPLUS AND CA
NEWS 12	Aug 23	Adis Newsletters (ADISNEWS) now available on STN
NEWS 13	Sep 17	IMSworld Pharmaceutical Company Directory name change to PHARMASEARCH
NEWS 14	Oct 09	Korean abstracts now included in Derwent World Patents Index
NEWS 15	Oct 09	Number of Derwent World Patents Index updates increased
NEWS 16	Oct 15	Calculated properties now in the REGISTRY/ZREGISTRY File
NEWS 17	Oct 22	Over 1 million reactions added to CASREACT
NEWS 18	Oct 22	DGENE GETSIM has been improved
NEWS 19	Oct 29	AAASD no longer available
NEWS 20	Nov 19	New Search Capabilities USPATFULL and USPAT2
NEWS 21	Nov 19	TOXCENTER(SM) - new toxicology file now available on STN
NEWS 22	Nov 29	COPPERLIT now available on STN
NEWS 23	Nov 29	DWPI revisions to NTIS and US Provisional Numbers
NEWS 24	Nov 30	Files VETU and VETB to have open access
NEWS 25	Dec 10	WPINDEX/WPIDS/WPIX New and Revised Manual Codes for 2002
NEWS 26	Dec 10	DGENE BLAST Homology Search
NEWS 27	Dec 17	WELDASEARCH now available on STN
NEWS 28	Dec 17	STANDARDS now available on STN
NEWS 29	Dec 17	New fields for DPCI
NEWS 30	Dec 19	CAS Roles modified
NEWS 31	Dec 19	1907-1946 data and page images added to CA and CAplus

NEWS EXPRESS	August 15 CURRENT WINDOWS VERSION IS V6.0c, CURRENT MACINTOSH VERSION IS V6.0 (ENG) AND V6.0J (JP), AND CURRENT DISCOVER FILE IS DATED 07 AUGUST 2001
NEWS HOURS	STN Operating Hours Plus Help Desk Availability
NEWS INTER	General Internet Information
NEWS LOGIN	Welcome Banner and News Items
NEWS PHONE	Direct Dial and Telecommunication Network Access to STN
NEWS WWW	CAS World Wide Web Site (general information)

Enter NEWS followed by the item number or name to see news on that specific topic.

FILE 'HOME' ENTERED AT 11:27:54 ON 11 JAN 2002

=> file .biotech

COST IN U.S. DOLLARS	SINCE FILE ENTRY	TOTAL SESSION
FULL ESTIMATED COST	0.15	0.15

FILE 'MEDLINE' ENTERED AT 11:28:09 ON 11 JAN 2002

FILE 'BIOSIS' ENTERED AT 11:28:09 ON 11 JAN 2002

FILE 'BIOTECHDS' ENTERED AT 11:28:09 ON 11 JAN 2002

FILE 'CAPLUS' ENTERED AT 11:28:09 ON 11 JAN 2002

FILE 'EMBASE' ENTERED AT 11:28:09 ON 11 JAN 2002

=> s transcri?
L1 981297 TRANSCRI?

=> s hybridiz?
L2 484866 HYBRIDIZ?

=> array
ARRAY IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> s array
L3 122090 ARRAY

=> s array or microarray or genechip
L4 129154 ARRAY OR MICROARRAY OR GENECHIP

=> s l1 and l2
L5 106937 L1 AND L2

=> s l4 and l5
L6 1721 L4 AND L5

=> s determin?
L7 4146108 DETERMIN?

=> s determin? or identif?
L8 6364125 DETERMIN? OR IDENTIF?

=> s l6 and l8
L9 889 L6 AND L8

=> s oligonucleotide?
L10 177281 OLIGONUCLEOTIDE?

```
=> s l9 and l10
L11         202 L9 AND L10

=> s transcri?  (a) region
L12        3031 TRANSCRI? (A) REGION

=> s l11 and l12
L13           0 L11 AND L12

=> s l12 and l3
L14          33 L12 AND L3

=> dup rem l14
PROCESSING COMPLETED FOR L14
L15          14 DUP REM L14 (19 DUPLICATES REMOVED)

=> d l14 ti

L14  ANSWER 1 OF 33      MEDLINE
TI   Two highly divergent 5S rDNA unit size classes occur in composite tandem
     array in European larch (Larix decidua Mill.) and Japanese larch
     (Larix kaempferi (Lamb.) Carr.).


=> d l14 ti 1-33

L14  ANSWER 1 OF 33      MEDLINE
TI   Two highly divergent 5S rDNA unit size classes occur in composite tandem
     array in European larch (Larix decidua Mill.) and Japanese larch
     (Larix kaempferi (Lamb.) Carr.).

L14  ANSWER 2 OF 33      MEDLINE
TI   Rat growth hormone gene introns stimulate nucleosome alignment in vitro
     and in transgenic mice.

L14  ANSWER 3 OF 33      MEDLINE
TI   DNA methylation status of the MUC1 gene coding for a breast-cancer-
     associated protein.

L14  ANSWER 4 OF 33      MEDLINE
TI   Regulatory autonomy and molecular characterization of the Drosophila out
     at first gene.

L14  ANSWER 5 OF 33      MEDLINE
TI   The Drosophila gene Serrate encodes an EGF-like transmembrane protein with
     a complex expression pattern in embryos and wing discs.

L14  ANSWER 6 OF 33      MEDLINE
TI   Characterization of VSG gene expression site promoters and
     promoter-associated DNA rearrangement events.

L14  ANSWER 7 OF 33      MEDLINE
TI   Chromatin structure at the replication origins and transcription-
     initiation regions of the ribosomal RNA genes of Tetrahymena.

L14  ANSWER 8 OF 33      MEDLINE
TI   Different nucleosome spacing in transcribed and non-transcribed regions of
     the ribosomal RNA gene in Tetrahymena thermophila.

L14  ANSWER 9 OF 33  BIOSIS  COPYRIGHT 2002 BIOSIS
TI   Two highly divergent 5S rDNA unit size classes occur in composite tandem
     array in European larch (Larix decidua Mill.) and Japanese larch
     (Larix kaempferi (Lamb.) Carr.
```

L14 ANSWER 10 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein.

L14 ANSWER 11 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice.

L14 ANSWER 12 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI Regulatory Autonomy and Molecular Characterization of the Drosophila out at first Gene.

L14 ANSWER 13 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI CHARACTERIZATION OF VSG GENE EXPRESSION SITE PROMOTERS AND PROMOTER-ASSOCIATED DNA REARRANGEMENT EVENTS.

L14 ANSWER 14 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI THE DROSOPHILA GENE SERRATE ENCODES AN EGF-LIKE TRANSMEMBRANE PROTEIN WITH A COMPLEX EXPRESSION PATTERN IN EMBRYOS AND WING DISCS.

L14 ANSWER 15 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI CHROMATIN STRUCTURE AT THE REPLICATION ORIGINS AND TRANSCRIPTION INITIATION REGIONS OF THE RIBOSOMAL RNA GENES OF TETRAHYMENA-THERMOPHILA.

L14 ANSWER 16 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Two highly divergent 5S rDNA unit size classes occur in composite tandem **array** in European larch (Larix decidua Mill.) and Japanese larch (Larix kaempferi (Lamb.) Carr.)

L14 ANSWER 17 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice

L14 ANSWER 18 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein

L14 ANSWER 19 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Interactions of the nucleoid-associated DNA-binding protein H-NS with the regulatory region of the osmotically controlled proU operon of Escherichia coli

L14 ANSWER 20 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Transcriptional mapping of the 3' end of the bovine syncytial virus genome

L14 ANSWER 21 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Proteolytic footprinting of transcription factor TFIIIA reveals different tightly binding sites for 5S RNA and 5S DNA

L14 ANSWER 22 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Balbiani ring 1 gene in Chironomus tentans. Sequence organization and dynamics of a coding minisatellite

L14 ANSWER 23 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a complex expression pattern in embryos and wing discs

L14 ANSWER 24 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Characterization of VSG gene expression site promoters and promoter-associated DNA rearrangement events

L14 ANSWER 25 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI The chromatin structure of hsp26

L14 ANSWER 26 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Chromatin structure at the replication origins and transcription-initiation regions of the ribosomal RNA genes of Tetrahymena

L14 ANSWER 27 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Replication in Paramecium mitochondrial DNA: functional sequence requirements in the origin region

L14 ANSWER 28 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Different nucleosome spacing in transcribed and nontranscribed regions of the ribosomal RNA gene in Tetrahymena thermophila

L14 ANSWER 29 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice.

L14 ANSWER 30 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein.

L14 ANSWER 31 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Regulatory autonomy and molecular characterization of the Drosophila out at first gene.

L14 ANSWER 32 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Characterization of VSG gene expression site promoters and promoter-associated DNA rearrangement events.

L14 ANSWER 33 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a complex expression pattern in embryos and wing discs.

=> d his

(FILE 'HOME' ENTERED AT 11:27:54 ON 11 JAN 2002)

FILE 'MEDLINE, BIOSIS, BIOTECHDS, CAPLUS, EMBASE' ENTERED AT 11:28:09 ON 11 JAN 2002

```
L1        981297 S TRANSCRI?
L2        484866 S HYBRIDIZ?
L3        122090 S ARRAY
L4        129154 S ARRAY OR MICROARRAY OR GENECHIP
L5        106937 S L1 AND L2
L6          1721 S L4 AND L5
L7       4146108 S DETERMIN?
L8       6364125 S DETERMIN? OR IDENTIF?
L9           889 S L6 AND L8
L10       177281 S OLIGONUCLEOTIDE?
L11          202 S L9 AND L10
L12         3031 S TRANSCRI?  (A) REGION
L13            0 S L11 AND L12
L14           33 S L12 AND L3
L15           14 DUP REM L14 (19 DUPLICATES REMOVED)
```

=> s l12 and l4
L16 33 L12 AND L4

=> d l16 ti 1-33

L16 ANSWER 1 OF 33 MEDLINE
TI Two highly divergent 5S rDNA unit size classes occur in composite tandem **array** in European larch (Larix decidua Mill.) and Japanese larch (Larix kaempferi (Lamb.) Carr.).

L16 ANSWER 2 OF 33 MEDLINE
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice.

L16 ANSWER 3 OF 33 MEDLINE
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein.

L16 ANSWER 4 OF 33 MEDLINE
TI Regulatory autonomy and molecular characterization of the Drosophila out at first gene.

L16 ANSWER 5 OF 33 MEDLINE
TI The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a complex expression pattern in embryos and wing discs.

L16 ANSWER 6 OF 33 MEDLINE
TI Characterization of VSG gene expression site promoters and promoter-associated DNA rearrangement events.

L16 ANSWER 7 OF 33 MEDLINE
TI Chromatin structure at the replication origins and transcription-initiation regions of the ribosomal RNA genes of Tetrahymena.

L16 ANSWER 8 OF 33 MEDLINE
TI Different nucleosome spacing in transcribed and non-transcribed regions of the ribosomal RNA gene in Tetrahymena thermophila.

L16 ANSWER 9 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI Two highly divergent 5S rDNA unit size classes occur in composite tandem **array** in European larch (Larix decidua Mill.) and Japanese larch (Larix kaempferi (Lamb.) Carr.

L16 ANSWER 10 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein.

L16 ANSWER 11 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice.

L16 ANSWER 12 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI Regulatory Autonomy and Molecular Characterization of the Drosophila out at first Gene.

L16 ANSWER 13 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI CHARACTERIZATION OF VSG GENE EXPRESSION SITE PROMOTERS AND PROMOTER-ASSOCIATED DNA REARRANGEMENT EVENTS.

L16 ANSWER 14 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI THE DROSOPHILA GENE SERRATE ENCODES AN EGF-LIKE TRANSMEMBRANE PROTEIN WITH A COMPLEX EXPRESSION PATTERN IN EMBRYOS AND WING DISCS.

L16 ANSWER 15 OF 33 BIOSIS COPYRIGHT 2002 BIOSIS
TI CHROMATIN STRUCTURE AT THE REPLICATION ORIGINS AND TRANSCRIPTION INITIATION REGIONS OF THE RIBOSOMAL RNA GENES OF TETRAHYMENA-THERMOPHILA.

L16 ANSWER 16 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Two highly divergent 5S rDNA unit size classes occur in composite tandem **array** in European larch (Larix decidua Mill.) and Japanese larch (Larix kaempferi (Lamb.) Carr.)

L16 ANSWER 17 OF 33 CAPLUS COPYRIGHT 2002 ACS

TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice

L16 ANSWER 18 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein

L16 ANSWER 19 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Interactions of the nucleoid-associated DNA-binding protein H-NS with the regulatory region of the osmotically controlled proU operon of Escherichia coli

L16 ANSWER 20 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Transcriptional mapping of the 3' end of the bovine syncytial virus genome

L16 ANSWER 21 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Proteolytic footprinting of transcription factor TFIIIA reveals different tightly binding sites for 5S RNA and 5S DNA

L16 ANSWER 22 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Balbiani ring 1 gene in Chironomus tentans. Sequence organization and dynamics of a coding minisatellite

L16 ANSWER 23 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI The Drosophila gene Serrate encodes an EGF-like transmembrane protein with a complex expression pattern in embryos and wing discs

L16 ANSWER 24 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Characterization of VSG gene expression site promoters and promoter-associated DNA rearrangement events

L16 ANSWER 25 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI The chromatin structure of hsp26

L16 ANSWER 26 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Chromatin structure at the replication origins and transcription-initiation regions of the ribosomal RNA genes of Tetrahymena

L16 ANSWER 27 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Replication in Paramecium mitochondrial DNA: functional sequence requirements in the origin region

L16 ANSWER 28 OF 33 CAPLUS COPYRIGHT 2002 ACS
TI Different nucleosome spacing in transcribed and nontranscribed regions of the ribosomal RNA gene in Tetrahymena thermophila

L16 ANSWER 29 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Rat growth hormone gene introns stimulate nucleosome alignment in vitro and in transgenic mice.

L16 ANSWER 30 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein.

L16 ANSWER 31 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Regulatory autonomy and molecular characterization of the Drosophila out at first gene.

L16 ANSWER 32 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI Characterization of VSG gene expression site promoters and promoter-associated DNA rearrangement events.

L16 ANSWER 33 OF 33 EMBASE COPYRIGHT 2002 ELSEVIER SCI. B.V.
TI The Drosophila gene Serrate encodes an EGF-like transmembrane protein with

a complex expression pattern in embryos and wing discs.

=> d ibib ab l16 18-21

L16 ANSWER 18 OF 33 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1995:755425 CAPLUS
DOCUMENT NUMBER: 123:220081
TITLE: DNA methylation status of the MUC1 gene coding for a breast-cancer-associated protein
AUTHOR(S): Zrihan-Licht, Sheila; Weiss, Mordechai; Keydar, Iafa; Wreschner, Daniel H.
CORPORATE SOURCE: Dep. of Cell Res. and Immunology, Tel Aviv University, Tel Aviv-Jaffa, 69978, Israel
SOURCE: Int. J. Cancer (1995), 62(3), 245-51
CODEN: IJCNAW; ISSN: 0020-7136
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The MUC1 gene codes for protein products that are highly expressed in human breast-cancer tissue and that serve as tumor markers for disease progression. The factors contributing to the disease-specific over-expression of the MUC1 gene are under intensive investigation and are yet to be detd. A large **transcribed region** of the human MUC1 gene is a CpG island that consists of 60-bp tandemly repeating units, each of which contains one SmaI restriction site. The methylation status of regulatory regions, upstream to the transcriptional start site, is essential for the regulation of gene expression. The authors therefore evaluated whether the methylation status of the various regions of the MUC1 gene may affect its expression. Using SmaI, and its isoschizomer XmaI endonucleases, the authors demonstrated that in peripheral-blood leukocytes (PBL-DNA) that do not express the MUC1 gene, the repeat **array** is completely methylated, whereas the same sequences are entirely non-methylated in breast-tumor-tissue DNA (BT-DNA). In contrast, sequences upstream and downstream to the repeat **array** showed no difference in the methylation pattern in PBL-DNA and BT-DNA. Hypomethylation within the repeat **array** was also obsd. in other epithelial tissues that express the MUC1 gene at much lower levels to those seen in breast-cancer tissue. These studies demonstrate that hypomethylation of the tandem repeat **array** is an abs. requirement for MUC1 gene expression in epithelial tissues, although in breast-cancer tissue addnl. regulatory mechanisms must pertain for its over-expression.

L16 ANSWER 19 OF 33 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:291286 CAPLUS
DOCUMENT NUMBER: 120:291286
TITLE: Interactions of the nucleoid-associated DNA-binding protein H-NS with the regulatory region of the osmotically controlled proU operon of Escherichia coli
AUTHOR(S): Lucht, Jan M.; Dersch, Petra; Kempf, Bettina; Bremer, Erhard
CORPORATE SOURCE: Dep. Biol., Univ. Konstanz, Konstanz, D-78434, Germany
SOURCE: J. Biol. Chem. (1994), 269(9), 6578-86
CODEN: JBCHA3; ISSN: 0021-9258
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The Escherichia coli hns gene encodes the abundant nucleoid-assocd. DNA-binding protein H-NS. Mutations in hns alter the expression of many genes with unrelated functions and result in a derepression of the proU operon (proVWX) without abolishing the osmotic control of its transcription. The authors have investigated the interactions of H-NS with the proU regulatory region by deletion anal. of cis-acting sequences, competitive gel retardation assays, and DNase I footprinting. The neg. effect of H-NS on proU transcription was mediated by cis-acting sequences

within proV but did not depend on the presence of a curved DNA segment upstream of the proU -35 region previously characterized as a target for H-NS binding in vitro. The authors detected a 46-base pair high affinity H-NS binding region downstream of the proU promoter at the 5' end of the proV gene and a complex **array** of addnl. H-NS binding sites which suggest the presence of an extended H-NS nucleoprotein complex. Most of the H-NS binding sites were highly A + T-rich and carried stretches of 5 or more consecutive A.cntdot.T base pairs. The implications of the authors' results for the osmotic regulation of proU transcription are discussed.

L16 ANSWER 20 OF 33 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1994:155320 CAPLUS
DOCUMENT NUMBER: 120:155320
TITLE: Transcriptional mapping of the 3' end of the bovine syncytial virus genome
AUTHOR(S): Renshaw, Randall W.; Casey, James W.
CORPORATE SOURCE: Coll. Vet. Med., Cornell Univ., Ithaca, NY, 14853, USA
SOURCE: J. Virol. (1994), 68(2), 1021-8
CODEN: JOVIAM; ISSN: 0022-538X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The bovine syncytial virus, a member of the retroviral subfamily Spumavirinae, causes a persistent asymptomatic infection in cattle. Nucleotide sequence anal. of the viral genome revealed two overlapping reading frames in the 3' region, traditionally occupied by accessory-function genes in other complex retroviruses. In order to analyze the transcripts from the accessory-gene region, the authors designed oligonucleotide primers complementary to sequences within the 5' and 3' long terminal repeats (LTRs) for use with the PCR. Southern blot anal. of amplification products revealed eight major cDNA bands. Eleven distinct cDNA clones were subsequently isolated and characterized. The initial splice donor in each clone is located 49 bp downstream from the mRNA cap site in the 5' LTR. The primary splice acceptor site was located 17 bp upstream from the proximal 3' open reading frame known as BF-ORF1. A second major splice acceptor was localized to a region upstream of the second open reading frame, BF-ORF2. Clones were identified which spliced directly to each of these sites. Addnl. splice donor and acceptor sites within BF-ORF1 and BF-ORF2 and the 3' LTR were variously used to generate a complex **array** of multiply spliced transcripts. Each of these transcripts remained in frame and coded for a potential protein product.

L16 ANSWER 21 OF 33 CAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1993:643693 CAPLUS
DOCUMENT NUMBER: 119:243693
TITLE: Proteolytic footprinting of transcription factor TFIIIA reveals different tightly binding sites for 5S RNA and 5S DNA
AUTHOR(S): Bogenhagen, Daniel F.
CORPORATE SOURCE: Dep. Pharmacol. Sci., State Univ. New York, Stony Brook, NY, 11794-8651, USA
SOURCE: Mol. Cell. Biol. (1993), 13(9), 5149-58
CODEN: MCEBD4; ISSN: 0270-7306
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Transcription factor IIIA (TFIIIA) employs an **array** of 9 N-terminal zinc fingers to bind specifically to both 5S RNA and 5S DNA. The binding of TFIIIA to 5S RNA and 5S DNA was studied by using a protease footprinting technique. Brief treatment of free or bound TFIIIA with trypsin or chymotrypsin generated fragments which were sepd. by sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Fragments retaining the N terminus of TFIIIA were identified by immunoblotting with an antibody directed against the N terminus of TFIIIA. Proteolytic footprinting of TFIIIA complexed with 5S DNA derivs. reinforced other

evidence that the 3 N-terminal zinc fingers of TFIIIA bind most tightly to 5S DNA. Proteolytic footprinting of TFIIIA in reconstituted 7S ribonucleoprotein particles revealed different patterns of trypsin sensitivity for TFIIIA bound to oocyte vs. somatic 5S RNA. Trypsin cleaved TFIIIA between zinc fingers 3 and 4 more readily when the protein was bound to somatic 5S RNA than when it was bound to oocyte 5S RNA. A tryptic fragment of TFIIIA contg. zinc fingers 4 through 7 remained tightly assocd. with somatic 5S RNA. Zinc fingers 4 through 7 may represent a tightly binding site for 5S RNA in the same sense that fingers 1 through 3 represent a tightly binding site for 5S DNA.

=> d ibib ab l11 1,2,10,13,57,79,99,100,107,108

L11 ANSWER 1 OF 202 MEDLINE
ACCESSION NUMBER: 2002004111 IN-PROCESS
DOCUMENT NUMBER: 21624570 PubMed ID: 11753363
TITLE: An integrated approach for finding overlooked genes in yeast.
AUTHOR: Kumar Anuj; Harrison Paul M; Cheung Kei-Hoi; Lan Ning; Echols Nathaniel; Bertone Paul; Miller Perry; Gerstein Mark B; Snyder Michael
CORPORATE SOURCE: Department of Molecular, Cellular, and Developmental Biology, Yale University, P.O. Box 208103, New Haven, CT 06520-8103.
SOURCE: NATURE BIOTECHNOLOGY, (2002 Jan 1) 20 (1) 58-63. Journal code: CQ3; 9604648. ISSN: 1087-0156.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20020102
Last Updated on STN: 20020102

AB We report here the discovery of 137 previously unappreciated genes in yeast through a widely applicable and highly scalable approach integrating methods of gene-trapping, **microarray**-based expression analysis, and genome-wide homology searching. Our approach is a multistep process in which expressed sequences are first trapped using a modified transposon that produces protein fusions to beta-galactosidase (beta-gal); non-annotated open reading frames (ORFs) translated as beta-gal chimeras are selected as a candidate pool of potential genes. To verify expression of these sequences, labeled RNA is **hybridized** against a **microarray** of **oligonucleotides** designed to detect gene **transcripts** in a strand-specific manner. In complement to this experimental method, novel genes are also **identified** in silico by homology to previously annotated proteins. As these methods are capable of **identifying** both short ORFs and antisense ORFs, our approach provides an effective supplement to current gene-finding schemes. In total, the genes discovered using this approach constitute 2% of the yeast genome and represent a wealth of overlooked biology.

L11 ANSWER 2 OF 202 MEDLINE
ACCESSION NUMBER: 2001671535 IN-PROCESS
DOCUMENT NUMBER: 21574174 PubMed ID: 11717296
TITLE: RNA Expression Analysis Using an Antisense Bacillus subtilis Genome **Array**.
AUTHOR: Lee J M; Zhang S; Saha S; Santa Anna S; Jiang C; Perkins J
CORPORATE SOURCE: Roche Vitamins Inc., Nutley, New Jersey 07110.
SOURCE: JOURNAL OF BACTERIOLOGY, (2001 Dec) 183 (24) 7371-80. Journal code: HH3; 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: IN-PROCESS; NONINDEXED; Priority Journals
ENTRY DATE: Entered STN: 20011122
Last Updated on STN: 20011122

AB We have developed an antisense **oligonucleotide** **microarray** for the study of gene expression and regulation in Bacillus subtilis by using Affymetrix technology. Quality control tests of the B. subtilis **GeneChip** were performed to ascertain the quality of the **array**. These tests included optimization of the labeling and **hybridization** conditions, **determination** of the linear dynamic range of gene expression levels, and assessment of differential gene expression patterns of known vitamin biosynthetic genes. In minimal medium, we detected **transcripts** for approximately 70%

of the known open reading frames (ORFs). In addition, we were able to monitor the **transcript** level of known biosynthetic genes regulated by riboflavin, biotin, or thiamine. Moreover, novel **transcripts** were also detected within intergenic regions and on the opposite coding strand of known ORFs. Several of these novel **transcripts** were subsequently correlated to new coding regions.

L11 ANSWER 10 OF 202 MEDLINE
ACCESSION NUMBER: 2001472744 MEDLINE
DOCUMENT NUMBER: 21178548 PubMed ID: 11282649
TITLE: Genomic interspecies **microarray hybridization**: rapid discovery of three thousand genes in the maize endophyte, Klebsiella pneumoniae 342, by **microarray hybridization** with Escherichia coli K-12 open reading frames.
AUTHOR: Dong Y; Glasner J D; Blattner F R; Triplett E W
CORPORATE SOURCE: Department of Agronomy, Wisconsin Gene Expression Center, University of Wisconsin-Madison, Madison, WI 53706, USA.
SOURCE: APPLIED AND ENVIRONMENTAL MICROBIOLOGY, (2001 Apr) 67 (4) 1911-21.
Journal code: 6K6; 7605801. ISSN: 0099-2240.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010827
Last Updated on STN: 20010827
Entered Medline: 20010823

AB In an effort to efficiently discover genes in the diazotrophic endophyte of maize, Klebsiella pneumoniae 342, DNA from strain 342 was **hybridized** to a **microarray** containing 96% (n = 4,098) of the annotated open reading frames from Escherichia coli K-12. Using a criterion of 55% identity or greater, 3,000 (70%) of the E. coli K-12 open reading frames were also found to be present in strain 342. Approximately 24% (n = 1,030) of the E. coli K-12 open reading frames are absent in strain 342. For 1.6% (n = 68) of the open reading frames, the signal was too low to make a **determination** regarding the presence or absence of the gene. Genes with high identity between the two organisms are those involved in energy metabolism, amino acid metabolism, fatty acid metabolism, cofactor synthesis, cell division, DNA replication, **transcription**, translation, transport, and regulatory proteins. Functions that were less highly conserved included carbon compound metabolism, membrane proteins, structural proteins, putative transport proteins, cell processes such as adaptation and protection, and central intermediary metabolism. Open reading frames of E. coli K-12 with little or no identity in strain 342 included putative regulatory proteins, putative chaperones, surface structure proteins, mobility proteins, putative enzymes, hypothetical proteins, and proteins of unknown function, as well as genes presumed to have been acquired by lateral transfer from sources such as phage, plasmids, or transposons. The results were in agreement with the physiological properties of the two strains. Whole genome comparisons by genomic interspecies **microarray hybridization** are shown to rapidly **identify** thousands of genes in a previously uncharacterized bacterial genome provided that the genome of a close relative has been fully sequenced. This approach will become increasingly more useful as more full genome sequences become available.

L11 ANSWER 13 OF 202 MEDLINE
ACCESSION NUMBER: 2001445860 MEDLINE
DOCUMENT NUMBER: 21374437 PubMed ID: 11481483
TITLE: Comparative expressed sequence **hybridization** to chromosomes for tumor classification and

identification of genomic regions of differential gene expression.
AUTHOR: Lu Y J; Williamson D; Clark J; Wang R; Tiffin N; Skelton L; Gordon T; Williams R; Allan B; Jackman A; Cooper C; Pritchard-Jones K; Shipley J
CORPORATE SOURCE: Molecular Cytogenetics, Institute of Cancer Research, Sutton, Surrey SM2 5NG, United Kingdom.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2001 Jul 31) 98 (16) 9197-202. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200108
ENTRY DATE: Entered STN: 20010813
Last Updated on STN: 20010903
Entered Medline: 20010830
AB Altered expression of genes can have phenotypic consequences in cancer development and treatment, developmental abnormalities, and differentiation processes. Here we describe a rapid approach, termed comparative expressed sequence **hybridization** (CESH), which gives a genome-wide view of relative expression patterns within tissues according to chromosomal location. No prior knowledge of genes or cloning is required, and minimal amounts of tissue can be used. Expression profiles are achieved in a manner similar to the **identification** of chromosomal imbalances by comparative genomic **hybridization** analysis. The approach is demonstrated to indicate a chromosomal region that harbors overexpressed genes that may be associated with a drug-resistant phenotype. In addition, known and new regions of differential gene expression in both normal tissues and tumor samples from the soft tissue sarcoma group of rhabdomyosarcoma (RMS) are indicated. These regions included 2p24; overexpression of MYCN at 2p24 was confirmed by quantitative reverse **transcription**-PCR for all of the alveolar RMS cases and did not necessarily correspond to genomic amplification. Evidence including region specific **microarray** analysis indicated that overexpression of several genes from a region may be required for detection by CESH. This evidence is consistent with clusters of functionally related genes and mechanisms that affect the expression of a number of genes at a particular genomic location. The distinctive CESH profiles demonstrated in different subtypes of RMS show potential for tumor classification.

L11 ANSWER 57 OF 202 MEDLINE
ACCESSION NUMBER: 2001212030 MEDLINE
DOCUMENT NUMBER: 21065211 PubMed ID: 11134512
TITLE: Model-based analysis of **oligonucleotide** arrays: expression index computation and outlier detection.
AUTHOR: Li C; Wong W H
CORPORATE SOURCE: Departments of Statistics and Human Genetics, University of California, Los Angeles, CA 90095.
CONTRACT NUMBER: 1R01HG02341-01 (NHGRI)
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (2001 Jan 2) 98 (1) 31-6. Journal code: PV3; 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200104
ENTRY DATE: Entered STN: 20010425
Last Updated on STN: 20010425
Entered Medline: 20010419
AB Recent advances in cDNA and **oligonucleotide** DNA arrays have made

it possible to measure the abundance of mRNA **transcripts** for many genes simultaneously. The analysis of such experiments is nontrivial because of large data size and many levels of variation introduced at different stages of the experiments. The analysis is further complicated by the large differences that may exist among different probes used to interrogate the same gene. However, an attractive feature of high-density **oligonucleotide** arrays such as those produced by photolithography and inkjet technology is the standardization of chip manufacturing and **hybridization** process. As a result, probe-specific biases, although significant, are highly reproducible and predictable, and their adverse effect can be reduced by proper modeling and analysis methods. Here, we propose a statistical model for the probe-level data, and develop model-based estimates for gene expression indexes. We also present model-based methods for **identifying** and handling cross-**hybridizing** probes and contaminating **array** regions. Applications of these results will be presented elsewhere.

L11 ANSWER 79 OF 202 MEDLINE
ACCESSION NUMBER: 2001046768 MEDLINE
DOCUMENT NUMBER: 20402107 PubMed ID: 10931279
TITLE: Global analysis of **transcription** kinetics during competence development in Streptococcus pneumoniae using high density DNA arrays.
AUTHOR: Rimini R; Jansson B; Feger G; Roberts T C; de Francesco M; Gozzi A; Faggioni F; Domenici E; Wallace D M; Frandsen N; Polissi A
CORPORATE SOURCE: Department of Microbiology, Glaxo Wellcome S.p.A., Verona, Italy.
SOURCE: MOLECULAR MICROBIOLOGY, (2000 Jun) 36 (6) 1279-92. Journal code: MOM. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200012
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001201

AB The kinetics of global changes in **transcription** patterns during competence development in Streptococcus pneumoniae was analysed with high-density arrays. Four thousand three hundred and one clones of a S. pneumoniae library, covering almost the entire genome, were amplified by PCR and gridded at high density onto nylon membranes. Competence was induced by the addition of CSP (competence stimulating peptide) to S. pneumoniae cultures grown to the early exponential phase. RNA was extracted from samples at 5 min intervals (for a period of 30 min) after the addition of CSP. Radiolabelled cDNA was generated from isolated total RNA by random priming and the probes were **hybridized** to identical high density arrays. Genes whose **transcription** was induced or repressed during competence were **identified**. Most of the genes previously known to be competence induced were detected together with several novel genes that all displayed the characteristic transient kinetics of competence-induced genes. Among the newly **identified** genes many have suggested functions compatible with roles in genetic transformation. Some of them may represent new members of the early or late competence regulons showing competence specific consensus sequences in their promoter regions. Northern experiments and mutational analysis were used to confirm some of the results.

L11 ANSWER 99 OF 202 MEDLINE
ACCESSION NUMBER: 1999412425 MEDLINE
DOCUMENT NUMBER: 99412425 PubMed ID: 10481021
TITLE: Genome-wide expression profiling in Escherichia coli K-12.
AUTHOR: Richmond C S; Glasner J D; Mau R; Jin H; Blattner F R

CORPORATE SOURCE: Laboratory of Genetics, University of Wisconsin, Madison, WI 53706, USA.. craig@genetics.wisc.edu
CONTRACT NUMBER: R01 GM35682 (NIGMS)
SOURCE: NUCLEIC ACIDS RESEARCH, (1999 Oct 1) 27 (19) 3821-35. Journal code: O8L; 0411011. ISSN: 1362-4962.
PUB. COUNTRY: ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199912
ENTRY DATE: Entered STN: 20000113 Last Updated on STN: 20010521 Entered Medline: 19991217

AB We have established high resolution methods for global monitoring of gene expression in Escherichia coli. **Hybridization** of radiolabeled cDNA to spot blots on nylon membranes was compared to **hybridization** of fluorescently-labeled cDNA to glass microarrays for efficiency and reproducibility. A complete set of PCR primers was created for all 4290 annotated open reading frames (ORFs) from the complete genome sequence of E.coli K-12 (MG1655). Glass- and nylon-based arrays of PCR products were prepared and used to assess global changes in gene expression. Full-length coding sequences for **array** printing were generated by two-step PCR amplification. In this study we measured changes in RNA levels after exposure to heat shock and following treatment with isopropyl-beta-D-thiogalactopyranoside (IPTG). Both radioactive and fluorescence-based methods showed comparable results. Treatment with IPTG resulted in high level induction of the lacZYA and melAB operons. Following heat shock treatment 119 genes were shown to have significantly altered expression levels, including 35 previously uncharacterized ORFs and most genes of the heat shock stimulon. Analysis of spot intensities from **hybridization** to replicate arrays **identified** sets of genes with signals consistently above background suggesting that at least 25% of genes were expressed at detectable levels during growth in rich media.

L11 ANSWER 100 OF 202 MEDLINE
ACCESSION NUMBER: 1999320744 MEDLINE
DOCUMENT NUMBER: 99320744 PubMed ID: 10392447
TITLE: Genome-wide **transcriptional** analysis in S. cerevisiae by mini-**array** membrane **hybridization**.
AUTHOR: Cox K H; Pinchak A B; Cooper T G
CORPORATE SOURCE: Department of Microbiology and Immunology, University of Tennessee, Memphis 38163, USA.
CONTRACT NUMBER: GM-35642 (NIGMS)
SOURCE: YEAST, (1999 Jun 15) 15 (8) 703-13. Journal code: YEA; 8607637. ISSN: 0749-503X.
PUB. COUNTRY: ENGLAND: United Kingdom Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199909
ENTRY DATE: Entered STN: 19990925 Last Updated on STN: 19990925 Entered Medline: 19990909

AB Access to the powerful micro-**array** analytical methods used for genome-wide **transcriptional** analysis has so far been restricted by the high cost and/or lack of availability of the sophisticated instrumentation and materials needed to perform it. Mini-**array** membrane **hybridization** provides a less expensive alternative. The reliability of this technique, however, is not well documented and its reported use has, up to this point, been very limited. Our objective was to test whether or not mini-**array** membrane **hybridization** would reliably **identify** genes whose expression was controlled by

a specific set of genetic and/or physiological signals. Our results demonstrate that mini-**array hybridization** can correctly **identify** genes whose expression is known to be controlled by the GATA-factor regulatory network in S. cerevisiae and in addition can reliably **identify** genes not previously reported to be associated with this nitrogen control system.

L11 ANSWER 107 OF 202 MEDLINE
ACCESSION NUMBER: 95238369 MEDLINE
DOCUMENT NUMBER: 95238369 PubMed ID: 7721781
TITLE: A haploid expressed gene cluster exists as a single chromatin domain in human sperm.
AUTHOR: Choudhary S K; Wykes S M; Kramer J A; Mohamed A N; Koppitch F; Nelson J E; Krawetz S A
CORPORATE SOURCE: Department of Obstetrics and Gynecology, Wayne State University School of Medicine, Detroit, Michigan 48201, USA.
CONTRACT NUMBER: 1RO1HD285040A1 (NICHD)
NO1-HD-0-2911 (NICHD)
SOURCE: JOURNAL OF BIOLOGICAL CHEMISTRY, (1995 Apr 14) 270 (15) 8755-62.
Journal code: HIV; 2985121R. ISSN: 0021-9258.
PUB. COUNTRY: United States
Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199505
ENTRY DATE: Entered STN: 19950605
Last Updated on STN: 19950605
Entered Medline: 19950519

AB Mammalian spermiogenesis is marked by the initial disruption of the nuclear-histone-DNA complex by the transition proteins for ultimate replacement with protamines. The genes for three of these low molecular weight basic nuclear proteins exist as a single linear **array** of PRM1, PRM2, and TNP2 on human chromosome 16p13.2. To begin to address the mechanism governing their **transcriptional** potentiation, a region of approximately 40 kilo-bases of the human genome encompassing these genes was introduced into the germ line of mice. Fluorescence in situ **hybridization** and Southern analysis showed that this segment of the human genome integrated into independent chromosomal sites while maintaining its fidelity. **Transcript** analysis demonstrated that the expression of the endogenous mouse protamine Prm1 and Prm2 genes as well as the mouse transition protein Tnp2 gene were expressed along with their human transgene counterparts. The pattern of expression of these transgenic human genes within this multigenic cluster faithfully represented that observed in vivo. In addition, all members of this transgenic gene cluster were expressed in proportions similar to those in human testis. Copy number-dependent and position-independent expression of the transgenic construct demonstrated that the corresponding biological locus was contained within this segment of the human genome. Furthermore, DNase I sensitivity established that in sperm the human PRM1-->PRM2-->TNP2 genic domain was contained as an approximately 28.5-kilobase contiguous segment bounded by an **array** of nuclear matrix associated topoisomerase II consensus sites. This is the first description of a multigenic male gamete-specific domain as a fundamental gene regulatory unit. A model of haploid-specific gene **determination** is presented.

L11 ANSWER 108 OF 202 BIOSIS COPYRIGHT 2002 BIOSIS
ACCESSION NUMBER: 2002:21855 BIOSIS
DOCUMENT NUMBER: PREV200200021855
TITLE: RNA expression analysis using an antisense Bacillus subtilis genome **array**.
AUTHOR(S): Lee, Jian-Ming; Zhang, Shehui; Saha, Soumitra; Santa Anna,

Sonia; Jiang, Can; Perkins, John (1)
CORPORATE SOURCE: (1) Department VFB, F. Hoffmann-La Roche, Ltd., Bldg. 203/20A, CH-4070, Basel: john.perkins@roche.com Switzerland
SOURCE: Journal of Bacteriology, (December, 2001) Vol. 183, No. 24, pp. 7371-7380. print.
ISSN: 0021-9193.
DOCUMENT TYPE: Article
LANGUAGE: English
AB We have developed an antisense **oligonucleotide microarray** for the study of gene expression and regulation in Bacillus subtilis by using Affymetrix technology. Quality control tests of the B. subtilis **GeneChip** were performed to ascertain the quality of the **array**. These tests included optimization of the labeling and **hybridization** conditions, **determination** of the linear dynamic range of gene expression levels, and assessment of differential gene expression patterns of known vitamin biosynthetic genes. In minimal medium, we detected **transcripts** for approximately 70% of the known open reading frames (ORFs). In addition, we were able to monitor the **transcript** level of known biosynthetic genes regulated by riboflavin, biotin, or thiamine. Moreover, novel **transcripts** were also detected within intergenic regions and on the opposite coding strand of known ORFs. Several of these novel **transcripts** were subsequently correlated to new coding regions

L4 ANSWER 1 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2001:290157 BIOSIS
DOCUMENT NUMBER: PREV200100290157
TITLE: Cloning and functional analysis of cDNAs with entire open reading frame for 300 previously undefined genes expressed in CD34+ hematopoietic stem/progenitor cells.
AUTHOR(S): Zhang, Q. H. (1); Ye, M. (1); Wu, X. Y. (1); Ren, S. X. (1); Chen, S. J. (1); Chen, Z. (1)
CORPORATE SOURCE: (1) Shanghai Institute of Hematology, Rui Jin Hospital, Shanghai Second Medical University, Shanghai China
SOURCE: Blood, (**November 16, 2000**) Vol. 96, No. 11 Part 2, pp. 130b. print.
Meeting Info.: 42nd Annual Meeting of the American Society of Hematology San Francisco, California, USA December 01-05, 2000 American Society of Hematology
. ISSN: 0006-4971.
DOCUMENT TYPE: Conference
LANGUAGE: English
SUMMARY LANGUAGE: English
ABSTRACT:
300 cDNAs containing putatively entire open reading frames (ORFs) for previously undefined genes were obtained from CD34+ hematopoietic stem/progenitor cells (HSPCs), based on EST cataloging, clone sequencing, in silico cloning and rapid amplification of cDNA ends (RACE). The cDNA sizes ranged from 360 to 3496 bp and their ORFs coded for peptides of 58 to 752 amino acids. Public database search indicated that 225 cDNAs exhibited sequence similarities to genes identified across a variety of species (bacteria, yeast, drosophila, arabidopsis and mammals not including primates). Homology analysis led to the recognition of 50 basic structure motifs/domains among these cDNAs. Genomic exon-intron organization could be established in 243 genes by integration of cDNA data with genome sequence information. Interestingly, a new gene named as HSPC070 on 3p was found to share a sequence of 105bp in 3'UTR with RAF gene in reversed **transcription** orientation. Chromosomal localizations were obtained using electronic mapping for 192 genes and with radiation hybrid (RH) for 38 ones. Macro-**array** technique was applied to screen the gene expression patterns in 5 hematopoietic cell lines (NB4, HL60, U937, K562 and Jurkat) and a number of genes with differential expression were found. The resource work has provided a wide range of information useful not only for expression genomics and **annotation** of genomic DNA sequence, but also for further research on the molecular regulation of hematopoietic development and differentiation. The biological functions of these previously undefined genes with regard to hematopoiesis are now under investigation.
CONCEPT CODE: Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
INDEX TERMS: Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Blood and Lymphatics (Transport and Circulation)
INDEX TERMS: Parts, Structures, & Systems of Organisms
CD34-positive hematopoietic stem/progenitor cells: blood and lymphatics
INDEX TERMS: Chemicals & Biochemicals
complementary DNA
INDEX TERMS: Methods & Equipment
complementary DNA cloning: genetic method; complementary

DNA functional analysis: analytical method, genetic method

INDEX TERMS: Miscellaneous Descriptors
gene expression; genomic exon-intron organization; open reading frame; Meeting Abstract

ORGANISM: Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGANISM: Organism Name
HL60 cell line (Hominidae); Jurkat cell line (Hominidae); K562 cell line (Hominidae); NB4 cell line (Hominidae); U937 cell line (Hominidae)

ORGANISM: Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L4 ANSWER 2 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS

ACCESSION NUMBER: 2001:50005 BIOSIS

DOCUMENT NUMBER: PREV200100050005

TITLE: Gene discovery using computational and microarray analysis of **transcription** in the Drosophila melanogaster testis.

AUTHOR(S): Andrews, Justen; Bouffard, Gerard G.; Cheadle, Chris; Lu, Jining; Becker, Kevin G.; Oliver, Brian (1)

CORPORATE SOURCE: (1) Laboratory of Cellular and Developmental Biology, National Institute of Diabetes and Digestive and Kidney Diseases, National Institutes of Health, Bethesda, MD, 20892: oliver@helix.nih.gov USA

SOURCE: Genome Research, (**December, 2000**) Vol. 10, No. 12, pp. 2030-2043. print.
ISSN: 1088-9051.

DOCUMENT TYPE: Article

LANGUAGE: English

SUMMARY LANGUAGE: English

ABSTRACT:
Identification and **annotation** of all the genes in the sequenced Drosophila genome is a work in progress. Wild-type testis function requires many genes and is thus of potentially high value for the identification of ***transcription*** units. We therefore undertook a survey of the repertoire of genes expressed in the Drosophila testis by computational and microarray analysis. We generated 3141 high-quality testis expressed sequence tags (ESTs). Testis ESTs computationally collapsed into 1560 cDNA set used for further analysis. Of those, 11% correspond to named genes, and 33% provide biological evidence for a predicted gene. A surprising 47% fail to align with existing ESTs and 16% with predicted genes in the current genome release. EST frequency and microarray expression profiles indicate that the testis mRNA population is highly complex and shows an extended range of **transcript** abundance. Furthermore, >80% of the genes expressed in the testis showed onefold overexpression relative to ovaries, or gonadectomized flies. Additionally, >3% showed more than threefold overexpression at $p<0.05$. Surprisingly, 22% of the genes most highly overexpressed in testis match Drosophila genomic sequence, but not predicted genes. These data strongly support the idea that sequencing additional cDNA libraries from defined tissues, such as testis, will be important tools for refined **annotation** of the Drosophila genome. Additionally, these data suggest that the number of genes in Drosophila will significantly exceed the conservative estimate of 13,601.

CONCEPT CODE: Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Reproductive System - Physiology and Biochemistry *16504
Invertebrata, Comparative and Experimental Morphology, Physiology and Pathology - Insecta - Physiology *64076

INDEX TERMS: Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques

INDEX TERMS: Parts, Structures, & Systems of Organisms
testis: reproductive system
INDEX TERMS: Chemicals & Biochemicals
cDNA [complementary DNA]; expressed sequence tags; mRNA [messenger RNA]
INDEX TERMS: Methods & Equipment
computational analysis: Mathematical and Computer Techniques, mathematical method; micro **array** techniques: genetic analysis, genetic method
INDEX TERMS: Miscellaneous Descriptors
transcription
ORGANISM: Super Taxa
Diptera: Insecta, Arthropoda, Invertebrata, Animalia
ORGANISM: Organism Name
Drosophila melanogaster (Diptera)
ORGANISM: Organism Superterms
Animals; Arthropods; Insects; Invertebrates

L4 ANSWER 3 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:430423 BIOSIS
DOCUMENT NUMBER: PREV200000430423
TITLE: Genome-wide protein interaction maps using two-hybrid systems.
AUTHOR(S): Legrain, Pierre (1); Selig, Luc
CORPORATE SOURCE: (1) Hybrigenics, 180 Avenue Daumesnil, Paris, 75012 France
SOURCE: FEBS Letters, (**25 August, 2000**) Vol. 480, No. 1, pp. 32-36. print.
ISSN: 0014-5793.
DOCUMENT TYPE: General Review
LANGUAGE: English
SUMMARY LANGUAGE: English
ABSTRACT:
Automated sequence technology has rendered functional biology amenable to genomic scale analysis. Among genome-wide exploratory approaches, the two-hybrid system in yeast (Y2H) has outranked other techniques because it is the system of choice to detect protein-protein interactions. Deciphering the cascade of binding events in a whole cell helps define signal transduction and metabolic pathways or enzymatic complexes. The function of proteins is eventually attributed through whole cell protein interaction maps where totally unknown proteins are partnered with fully **annotated** proteins belonging to the same functional category. Since its first description in the late 1980's, several versions of the Y2H have been developed in order to overcome the major limitations of the system, namely false positives and false negatives. Optimized versions have been recently applied at multi-molecular and genomic scale. These genome-wide surveys can be methodologically divided into two types of approaches: one either tests combinations of predefined polypeptides (the so-called matrix approach) using various short-cuts to speed up the process, or one screens with a given polypeptide (bait) for potential partners (preys) present in complex libraries of genomic or complementary DNA (library screening). In the former strategy, one tests what one knows, for example pair-wise interactions between full-length open reading frames from recently sequenced and **annotated** genomes. Although based on a one-by-one scheme, this method is reported to be amenable to large-scale genomics thanks to multicloning strategies and to the use of small robotics workstations. In the latter, highly complex cDNA or genomic libraries of protein domains can be screened to saturation with high-throughput screening systems allowing the discovery of yet unidentified proteins. Both approaches have strengths and drawbacks that will be discussed here. None yields a full proteome-wide screening since certain proteins (e.g. some **transcription** factors) are not usable in Y2H. Novel two-hybrid assays have been recently described in bacteria. Applications of these time- and cost-effective assays to genomic screening will be discussed and compared to the Y2H technology.
CONCEPT CODE: Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Plant *03504

Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
INDEX TERMS: Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
INDEX TERMS: Chemicals & Biochemicals
DNA
INDEX TERMS: Methods & Equipment
bacterial two-hybrid system: molecular genetic method; cDNA library screening: molecular genetic method; genome-wide protein interaction maps: molecular genetic method; protein **array**: analytical method; yeast two-hybrid system: molecular genetic method
INDEX TERMS: Miscellaneous Descriptors
biological network; functional genomics
ORGANISM: Super Taxa
Ascomycetes: Fungi, Plantae
ORGANISM: Organism Name
Saccharomyces cerevisiae (Ascomycetes)
ORGANISM: Organism Superterms
Fungi; Microorganisms; Nonvascular Plants; Plants

L4 ANSWER 4 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:387625 BIOSIS
DOCUMENT NUMBER: PREV200000387625
TITLE: Identification of novel human genes evolutionarily conserved in Caenorhabditis elegans by comparative proteomics.
AUTHOR(S): Lai, Chun-Hung; Chou, Chang-Yuan; Ch'ang, Lan-Yang; Liu, Chung-Shyan; Lin, Wen-chang (1)
CORPORATE SOURCE: (1) Institute of Biomedical Sciences, Academia Sinica, Taipei, 115 Taiwan
SOURCE: Genome Research, (**May, 2000**) Vol. 10, No. 5, pp. 703-713. print.
ISSN: 1088-9051.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
ABSTRACT:
Modern biomedical research greatly benefits from large-scale genome-sequencing projects ranging from studies of viruses, bacteria, and yeast to multicellular organisms, like Caenorhabditis elegans. Comparative genomic studies offer a vast **array** of prospects for identification and functional ***annotation*** of human ortholog genes. We presented a novel comparative proteomic approach for assembling human gene contigs and assisting gene discovery. The C. elegans proteome was used as an alignment template to assist in novel human gene identification from human EST nucleotide databases. Among the available 18,452 C. elegans protein sequences, our results indicate that at least 83% (15,344 sequences) of C. elegans has human homologous genes, with 7,954 records of C. elegans proteins matching known human gene ***transcripts*** . Only 11% or less of C. elegans proteome contains nematode-specific genes. We found that the remaining 7,390 sequences might lead to discoveries of novel human genes, and over 150 putative full-length human gene **transcripts** were assembled upon further database analyses.
CONCEPT CODE: Evolution *01500
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
Invertebrata, Comparative and Experimental Morphology, Physiology and Pathology - Aschelminthes *64016
INDEX TERMS: Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Evolution and Adaptation; Methods and Techniques
INDEX TERMS: Chemicals & Biochemicals
human genes; Caenorhabditis elegans genes (Nematoda)
INDEX TERMS: Methods & Equipment

comparative genomics: Molecular Biology Techniques and Chemical Characterization, molecular genetic method; comparative proteomics: Molecular Biology Techniques and Chemical Characterization, analytical method

ORGANISM: Super Taxa
Nematoda: Aschelminthes, Helminthes, Invertebrata, Animalia

ORGANISM: Organism Name
Caenorhabditis elegans (Nematoda)

ORGANISM: Organism Superterms
Animals; Aschelminths; Helminths; Invertebrates

L4 ANSWER 5 OF 5 BIOSIS COPYRIGHT 2001 BIOSIS
ACCESSION NUMBER: 2000:88513 BIOSIS
DOCUMENT NUMBER: PREV200000088513
TITLE: The Genexpress IMAGE Knowledge Base of the human muscle **transcriptome**: A resource of structural, functional, and positional candidate genes for muscle physiology and pathologies.
AUTHOR(S): Pietu, Genevieve (1); Eveno, Eric; Soury-Segurens, Beatrice; Fayein, Nicole-Adeline; Mariage-Samson, Regine; Matingou, Christiane; Leroy, Elisabeth; Dechesne, Claude; Krieger, Sabine; Ansorge, Wilhelm; Reguigne-Arnould, Isabelle; Cox, David; Dehejia, Anindya; Polymeropoulos, Mihael H.; Devignes, Marie-Dominique; Auffray, Charles
CORPORATE SOURCE: (1) Genexpress, Centre National de la Recherche Scientifique (CNRS) ERS 1984, 94801, Villejuif France
SOURCE: Genome Research, (**Dec.**, **1999**) Vol. 9, No. 12, pp. 1313-1320.
ISSN: 1088-9051.
DOCUMENT TYPE: Article
LANGUAGE: English
SUMMARY LANGUAGE: English
ABSTRACT:
Sequence, gene mapping, and expression data corresponding to 910 genes transcribed in human skeletal muscle have been integrated to form the muscle module of the Genexpress IMAGE Knowledge Base. Based on cDNA **array** hybridization, a set of 14 **transcripts** preferentially or specifically expressed in muscle have been selected and characterized in more detail: Their pattern of expression was confirmed by Northern blot analysis; their structure was further characterized by full-insert cDNA sequencing and cDNA extension; the map location of the corresponding genes was refined by radiation hybrid mapping. Five of the 14 selected genes appear as interesting positional and functional candidate genes to study in relation with muscle physiology and/or specific orphan muscular pathologies. One example is discussed in more detail. The expression profilling data and the associated Genexpress Index2 entries for the 910 genes and the detailed characterization of the 14 selected ***transcripts*** are available from a dedicated Web server at http://idefix.upr420.vjf.cnrs.fr/IMAGE/Page-unique/welcome-muscles.html. The database has been organized to provide the users with a working space where they can find curated, **annotated**, integrated data for their genes of interest. Different navigation routes to exploit the resource are discussed.
CONCEPT CODE: Genetics and Cytogenetics - General *03502
General Biology - Information, Documentation, Retrieval and Computer Applications *00530
Genetics and Cytogenetics - Human *03508
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Replication, Transcription, Translation *10300
Biophysics - Molecular Properties and Macromolecules *10506
Physiology, General and Miscellaneous - General *12002
Pathology, General and Miscellaneous - General *12502

	Metabolism - Nucleic Acids, Purines and Pyrimidines *13014
	Muscle - General; Methods *17501
BIOSYSTEMATIC CODE:	Hominidae 86215
INDEX TERMS:	Major Concepts
	Molecular Genetics (Biochemistry and Molecular Biophysics); Computer Applications (Computational Biology); Methods and Techniques; Muscular System (Movement and Support)
INDEX TERMS:	Parts, Structures, & Systems of Organisms
	muscles: muscular system
INDEX TERMS:	Chemicals & Biochemicals
	DNA: analysis, sequencing; cDNA [complementary DNA]: analysis, hybridization
INDEX TERMS:	Methods & Equipment
	DNA hybridization: Analysis/Characterization Techniques: CB, analytical method; gene mapping: analytical method, mapping techniques; gene sequencing: analytical method, cycle DNA sequencing
INDEX TERMS:	Miscellaneous Descriptors
	Genexpress IMAGE Knowledge Base: applications; gene expression: analysis; gene markers: analysis; pathology; physiology; **transcriptomes**: analysis, functions
ORGANISM:	Super Taxa
	Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGANISM:	Organism Name
	human (Hominidae)
ORGANISM:	Organism Superterms
	Animals; Chordates; Humans; Mammals; Primates; Vertebrates

=> fil biosis

FILE 'BIOSIS' ENTERED AT 12:10:48 ON 26 JAN 2001

FILE COVERS 1969 TO DATE.
CAS REGISTRY NUMBERS AND CHEMICAL NAMES (CNs) PRESENT
FROM JANUARY 1969 TO DATE.

RECORDS LAST ADDED: 24 January 2001 (20010124/ED)

The BIOSIS file has been reloaded. Enter HELP RLOAD and HELP REINDEXING
for details.

=> d all tot

L33 ANSWER 1 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:50006 BIOSIS
DN PREV200100050006
TI Detection of deleted **genomic DNA** using a semiautomated computational analysis of **GeneChip** data.
AU Salamon, Hugh (1); Kato-Maeda, Midori; Small, Peter M.; Drenkow, Jorg; **Gingeras, Thomas R.**
CS (1) Division of Infectious Diseases and Geographic Medicine, Department of Medicine, Stanford University, Stanford, CA, 94305: Hugh_Salamon@Berlex.com USA
SO Genome Research, (December, 2000) Vol. 10, No. 12, pp. 2044-2054. print. ISSN: 1088-9051.
DT Article
LA English
SL English
AB **Genomic** diversity within and between populations is caused by single nucleotide **mutations**, changes in repetitive **DNA** systems, recombination mechanisms, and insertion and deletion events. The contribution of these sources to diversity, whether purely **genetic** or of phenotypic consequence, can only be investigated if we have the means to quantitate and characterize diversity in many samples. With the advent of complete sequence characterization of representative **genomes** of different species, the possibility of developing protocols to screen for **genetic** polymorphism across entire **genomes** is actively being pursued. The large numbers of measurements such approaches yield demand that we pay careful attention to the numerical analysis of data. In this paper we present a novel application of an Affymetrix **GeneChip** to perform **genome** -wide screens for deletion polymorphism. A high-**density** **oligonucleotide array** formatted for mRNA expression and targeted at a fully sequenced 4.4-million-base pair Mycobacterium tuberculosis standard strain **genome** was adapted to compare **genomic DNA**. **Hybridization** intensities to 111,000 **probe** pairs (perfect complement and **mismatch** complement) were measured for **genomic DNA** from a clinical strain and from a vaccine organism. Because individual **probe**-pair **hybridization** intensities exhibit limited sensitivity/specificity characteristics to detect deletions, data-analytical methodology to exploit measurements from multiple **probes** in tandem locations across the **genome** was developed. The TSTEP (Tandem Set Terminal Extreme Probability) algorithm designed specifically to analyze the tandem **hybridization** measurements data was applied and shown to discover **genomic** deletions with high sensitivity. The TSTEP algorithm provides a foundation for similar efforts to characterize deletions in many **hybridization** measures in similar-sized and larger **genomes** . Issues relating to the design of **genome** content screening experiments and the implications of these methods for studying population **genomics** and the evolution of **genomes** are discussed.

CC **Genetics and Cytogenetics - General *03502**
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Chemicals & Biochemicals
DNA: analysis, **genomic**
IT Methods & Equipment
computational analysis: Mathematical and **Computer** Techniques, mathematical method
IT Miscellaneous Descriptors
GeneChip data; Tandem Set Terminal Extreme Probability algorithm
ORGN Super Taxa
Mycobacteriaceae: Mycobacteria, Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms
ORGN Organism Name
Mycobacterium tuberculosis (Mycobacteriaceae)
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms

L33 ANSWER 2 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:493432 BIOSIS
DN PREV200000493553
TI Single nucleotide polymorphism discovery in candidate **genes** for rheumatoid arthritis.
AU Hacker, C. (1); Thomas, D. (1); Doshi, J. (1); Kimberly, R. P.; **Gingeras, T. R. (1)**; Patil, N. (1)
CS (1) Affymetrix, Santa Clara, CA USA
SO American Journal of Human Genetics, (October, 2000) Vol. 67, No. 4 Supplement 2, pp. 335. print.
Meeting Info.: 50th Annual Meeting of the American Society of Human Genetics Philadelphia, Pennsylvania, USA October 03-07, 2000 American Society of Human Genetics
. ISSN: 0002-9297.
DT Conference
LA English
SL English
CC Bones, Joints, Fasciae, Connective and Adipose Tissue - Pathology *18006
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34508
Allergy *35500
IT Major Concepts
Genetics; Rheumatology (Human Medicine, Medical Sciences); Methods and Techniques
IT Diseases
rheumatoid arthritis: connective tissue disease, immune system disease, joint disease
IT Chemicals & Biochemicals
rheumatoid arthritis candidate **genes** (Hominidae): single nucleotide polymorphism discovery
IT Alternate Indexing
Arthritis, Rheumatoid (MeSH)
IT Methods & Equipment
GeneChip-Registered Trademark **probe arrays**
: analytical method, **genetic** method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Poster
ORGN Super Taxa

different **oligonucleotide** is localized in a predetermined region of the surface, the **density** of the different **oligonucleotides** is greater than about 60 different **oligonucleotides** per 1 cm2, and the olignucleotide **probes** are complementary to the RNA **transcripts** or **nucleic acids** derived from the RNA **transcripts**; and quantifying the **hybridized nucleic acids** in the **array.**

NCL 435006000

IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics); Methods and Techniques

IT Chemicals & Biochemicals
RNA; high **density oligonucleotide arrays; nucleic acids**

IT Methods & Equipment
high **density oligonucleotide arrays-hybridization** method: monitoring method

IT Miscellaneous Descriptors
gene multiplicity

L33 ANSWER 5 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2000:398753 BIOSIS

DN PREV200000398753

TI Use of high **density oligonucleotide arrays** to assist in **transcriptional** annotation of the **E. coli genome.**

AU **Rosenow, C. I. (1)**; Saxena, R. Mukherjee (1); **Gingeras, T. (1)**

CS (1) Affymetrix, Santa Clara, CA USA

SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 446. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology Los Angeles, California, USA May 21-25, 2000 American Society for Microbiology
. ISSN: 1060-2011.

DT Conference

LA English

SL English

CC Physiology and Biochemistry of Bacteria *31000
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Genetics of Bacteria and Viruses *31500
Virology - Bacteriophage *33504

BC Bacterial Viruses - General 02700

IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics)

IT Chemicals & Biochemicals
RNA

IT Methods & Equipment
high **density oligonucleotide arrays:** analytical method, **genetic** method

IT Miscellaneous Descriptors
Escherichia coli genome: transcriptional annotation; bacterial **genetics;** Meeting Abstract; Meeting Poster

ORGN Super Taxa
Bacterial Viruses: Viruses, Microorganisms; **Enterobacteriaceae: Facultatively Anaerobic Gram-Negative Rods, Eubacteria, Bacteria, Microorganisms**

ORGN Organism Name
Escherichia coli (Enterobacteriaceae); bacteriophage (Bacterial Viruses)

ORGN Organism Superterms
Bacteria; Bacterial Viruses; Eubacteria; Microorganisms; Viruses

L33 ANSWER 6 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:324396 BIOSIS
DN PREV200000324396
TI Monitoring **gene** expression using **DNA microarrays**.
AU Harrington, Christina A. (1); **Rosenow, Carsten (1)**; Retief, Jacques (1)
CS (1) Affymetrix, Inc., 3380 Central Expressway, Santa Clara, CA, 95051 USA
SO Current Opinion in Microbiology, (June, 2000) Vol. 3, No. 3, pp. 285-291. print.
ISSN: 1369-5274.
DT General Review
LA English
SL English
AB The concurrent development of high-**density array** technologies and the complete sequencing of a number of microbial **genomes** is providing the opportunity to comprehensively and efficiently survey the **transcription** profile of microorganisms under different conditions and well-defined genotypes. **Microarray** -based studies are uncovering broad patterns of **genetic** activity, providing new understanding of **gene** functions and, in some cases, generating unexpected insight into **transcriptional** processes and biological mechanisms. One topic that has come to the forefront is how best to effectively manage and interpret the large data sets being generated. Although progress has been made, this remains a challenging opportunity for functional **genomics** research.
CC **Genetics and Cytogenetics - General *03502**
IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Chemicals & Biochemicals
gene: function; microbial **genome**
IT Methods & Equipment
DNA microarray: equipment; high-**density array** technology: equipment; **microarray**-based studies: analytical method
IT Miscellaneous Descriptors
biological mechanisms; broad **genetic** activity patterns; functional **genomics** research; large data sets: interpretation; **transcription** profile; **transcriptional** processes

L33 ANSWER 7 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:314021 BIOSIS
DN PREV200000314021
TI **Nucleic acid** affinity columns.
AU Lipshutz, Robert J. (1); Morris, MacDonald S.; Chee, Mark S.; **Gingeras, Thomas R.**
CS (1) Palo Alto, CA USA
ASSIGNEE: Affymetrix, Inc., Santa Clara, CA, USA
PI US 6013440 January 11, 2000
SO Official Gazette of the United States Patent and Trademark Office Patents, (Jan. 11, 2000) Vol. 1230, No. 2, pp. No pagination. e-file.
ISSN: 0098-1133.
DT Patent
LA English
AB This invention provides **nucleic acid** affinity matrices that bear a large number of different **nucleic acid** affinity ligands allowing the simultaneous selection and removal of a large number of preselected **nucleic acids** from the sample. Methods of producing such affinity matrices are also provided. In general the methods involve the steps of a) providing a **nucleic acid** amplification template **array** comprising a surface

to which are attached at least 50 **oligonucleotides** having different **nucleic acid** sequences, and wherein each different **oligonucleotide** is localized in a predetermined region of said surface, the **density** of said **oligonucleotides** is greater than about 60 different **oligonucleotides** per 1 cm2, and all of said different **oligonucleotides** have an identical terminal 3' **nucleic acid** sequence and an identical terminal 5' **nucleic acid** sequence. b) amplifying said multiplicity of **oligonucleotides** to provide a pool of amplified **nucleic acids**; and c) attaching the pool of **nucleic acids** to a solid support.

NCL 435006000

IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics); Methods and Techniques

IT Methods & Equipment
production of **nucleic acid** affinity columns: amplification method

IT Miscellaneous Descriptors
nucleic acid affinity matrices

L33 ANSWER 8 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2000:229566 BIOSIS

DN PREV200000229566

TI Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse.

AU Lindblad-Toh, Kerstin (1); Winchester, Ellen; Daly, Mark J.; Wang, David G.; Hirschhorn, Joel N.; Laviolette, Jean-Philippe; Ardlie, Kristin; Reich, David E.; Robinson, Elizabeth; Sklar, Pamela; Shah, Nila; Thomas, Daryl; Fan, Jian-Bing; **Gingeras, Thomas**; Warrington, Janet; Patil, Nila; Hudson, Thomas J.; Lander, Eric S. (1)

CS (1) MIT Center for Genome Research, Whitehead Institute, Whitehead Institute for Biomedical Research, Cambridge, MA USA

SO Nature Genetics, (April, 2000) Vol. 24, No. 4, pp. 381-386. ISSN: 1061-4036.

DT Article

LA English

SL English

AB Single-nucleotide polymorphisms (SNPs) have been the focus of much attention in human **genetics** because they are extremely abundant and well-suited for automated large-scale genotyping. Human SNPs, however, are less informative than other types of **genetic** markers (such as simple-sequence length polymorphisms or microsatellites) and thus more loci are required for mapping traits. SNPs offer similar advantages for experimental **genetic** organisms such as the mouse, but they entail no loss of informativeness because bi-allelic markers are fully informative in analysing crosses between inbred strains. Here we report a large-scale analysis of SNPs in the mouse **genome**. We characterized the rate of nucleotide polymorphism in eight mouse strains and identified a collection of 2,848 SNPs located in 1,755 sequence-tagged sites (STSs) using high-**density oligonucleotide arrays**. Three-quarters of these SNPs have been mapped on the mouse **genome**, providing a first-generation SNP map of the mouse. We have also developed a multiplex genotyping procedure by which a **genome** scan can be performed with only six genotyping reactions per animal.

CC **Genetics and Cytogenetics - Animal *03506**

IT Major Concepts
Genetics

IT Miscellaneous Descriptors
single-nucleotide polymorphism: genotyping, large-scale discovery

ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
mouse (Muridae)

ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates;

Rodents; Vertebrates

L33 ANSWER 9 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:96995 BIOSIS
DN PREV199900096995
TI **Array** of **nucleic acid probes** on biological **chips** for diagnosis of HIV and methods of using the same.
AU Chee, M.; **Gingeras, T. R.**; Fodor, S. P. A.; Hubble, E. A.; Morris, M. S.
CS Palo Alto, Calif. USA
ASSIGNEE: AFFYMETRIX, INC.
PI US 5861242 Jan. 19, 1999
SO Official Gazette of the United States Patent and Trademark Office Patents, (Jan. 19, 1999) Vol. 1218, No. 3, pp. 2170.
ISSN: 0098-1133.
DT Patent
LA English
NCL 435005000
CC **Mathematical Biology and Statistical Methods** *04500
*15900
*27100
*51300
*52100
*52500
*72100
*80100
IT Major Concepts
Biochemistry and Molecular Biophysics; General Life Studies; **Genetics**; Immune System (Chemical Coordination and Homeostasis); Infection; Methods and Techniques; Pathology
IT Miscellaneous Descriptors
ACQUIRED IMMUNE DEFICIENCY SYNDROME; AIDS; BIOTECHNOLOGY; DIAGNOSTIC TESTING; IMMUNOASSAY; MEDICAL DIAGNOSTICS; **OLIGONUCLEOTIDE PROBES**
ORGN Super Taxa
Retroviridae: Viruses
ORGN Organism Name
human immunodeficiency virus (Retroviridae); microorganism (Microorganisms - Unspecified)
ORGN Organism Superterms
microorganisms; viruses

L33 ANSWER 10 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:53632 BIOSIS
DN PREV199900053632
TI Mycobacterium species identification and rifampin resistance testing with high-**density DNA probe arrays**.
AU Troesch, A. (1); Nguyen, H.; Miyada, C. G.; Desvarenne, S.; **Gingeras, T. R.**; Kaplan, P. M.; Cros, P.; Mabilat, C.
CS (1) Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051 USA
SO Journal of Clinical Microbiology, (Jan., 1999) Vol. 37, No. 1, pp. 49-55.
ISSN: 0095-1137.
DT Article
LA English
AB Species identification within the genus Mycobacterium and subsequent antibiotic susceptibility testing still rely on time-consuming, culture-based methods. Despite the recent development of **DNA probes**, which greatly reduce assay time, there is a need for a single platform assay capable of answering the multitude of diagnostic questions associated with this genus. We describe the use of a **DNA probe array** based on two sequence **databases**: one for the species identification of mycobacteria (82 unique 16S rRNA sequences corresponding to 54 phenotypical species) and the other for detecting Mycobacterium tuberculosis rifampin resistance (rpoB alleles). Species identification or rifampin resistance was determined by

hybridizing fluorescently labeled, amplified **genetic** material generated from bacterial colonies to the **array**. Seventy mycobacterial isolates from 27 different species and 15 rifampin-resistant M. tuberculosis strains were tested. A total of 26 of 27 species were correctly identified as well as all of the rpoB **mutants**. This parallel testing format opens new perspectives in terms of patient management for bacterial diseases by allowing a number of **genetic** tests to be simultaneously run.

CC Medical and Clinical Microbiology - General; Methods and Techniques *36001
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Genetics of Bacteria and Viruses *31500
Medical and Clinical Microbiology - Bacteriology *36002
Chemotherapy - Antibacterial Agents *38504
BC Mycobacteriaceae 08881
IT Major Concepts
Bacteriology; Methods and Techniques; Pharmacology
IT Chemicals & Biochemicals
rifampin: antibacterial - drug, resistance; 16S ribosomal RNA
IT Methods & Equipment
antimicrobial resistance testing: analytical method; high-**density DNA probe array**
technique: analytical method
ORGN Super Taxa
Mycobacteriaceae: Mycobacteria, Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms
ORGN Organism Name
Mycobacterium tuberculosis (Mycobacteriaceae): identification, pathogen
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms
RN 13292-46-1 (RIFAMPIN)

L33 ANSWER 11 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:8586 BIOSIS
DN PREV199900008586
TI Cellular **gene** expression altered by human cytomegalovirus: Global monitoring with **oligonucleotide arrays**.
AU Zhu, Hua; Cong, Jian-Ping; Mamitora, Gargi; **Gingeras, Thomas**; Shenk, Thomas (1)
CS (1) Howard Hughes Med. Inst., Dep. Mol. Biol., Princeton Univ., Priinceton, NJ 08544 USA
SO Proceedings of the National Academy of Sciences of the United States of America, (Nov. 24, 1998) Vol. 95, No. 24, pp. 14470-14475. ISSN: 0027-8424.
DT Article
LA English
AB Mechanistic insights to viral replication and pathogenesis generally have come from the analysis of viral **gene** products, either by studying their biochemical activities and interactions individually or by creating **mutant** viruses and analyzing their phenotype. Now it is possible to identify and catalog the host cell **genes** whose mRNA levels change in response to a pathogen. We have used **DNA array** technology to monitor the level of apprxeq6,600 human mRNAs in uninfected as compared with human cytomegalovirus-infected cells. The level of 258 mRNAs changed by a factor of 4 or more before the onset of viral **DNA** replication. Several of these mRNAs encode **gene** products that might play key roles in virus-induced pathogenesis, identifying them as intriguing targets for further study.
CC **Genetics and Cytogenetics - Human *03508**
Genetics of Bacteria and Viruses *31500
Medical and Clinical Microbiology - General; Methods and Techniques *36001
BC Herpesviridae 02612
Hominidae 86215
IT Major Concepts

Infection; Molecular **Genetics** (Biochemistry and Molecular Biophysics)
IT Methods & Equipment
global monitoring: **genetic** method; **oligonucleotide array**: **genetic** method
IT Miscellaneous Descriptors
cellular **gene** expression
ORGN Super Taxa
Herpesviridae: Animal Viruses, Viruses, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): host; human cytomegalovirus (Herpesviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L33 ANSWER 12 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:415378 BIOSIS
DN PREV199800415378
TI Drug resistance and species identification in Mycobacterium infections greater than using **oligonucleotide arrays**.
AU **Gingeras, Thomas R. (1)**; Ghandour, Ghassan (1); Wang, Eugene (1); Berno, Anthony (1); Small, Peter M.; Drobniewski, Francis; Alland, David; Desmond, Edward; Holodniy, M.; Drenkow, J. (1)
CS (1) Affymetrix, Santa Clara, CA USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (1998) Vol. 98, pp. 18.
Meeting Info.: 98th General Meeting of the American Society for Microbiology Atlanta, Georgia, USA May 17-21, 1998 American Society for Microbiology
. ISSN: 1060-2011.
DT Conference
LA English
CC Medical and Clinical Microbiology - Bacteriology *36002
Biochemical Studies - General *10060
Genetics of Bacteria and Viruses *31500
Chemotherapy - Antibacterial Agents *38504
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Mycobacteriaceae 08881
IT Major Concepts
Infection; Pharmacology
IT Diseases
mycobacterium infection: bacterial disease
IT Chemicals & Biochemicals
rifampin: antibacterial - drug, resistance; rpoB **gene**
IT Miscellaneous Descriptors
drug resistance; **DNA** sequence; Meeting Abstract
ORGN Super Taxa
Mycobacteriaceae: Mycobacteria, Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms
ORGN Organism Name
Mycobacterium-tuberculosis (Mycobacteriaceae): pathogen
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms
RN 13292-46-1 (RIFAMPIN)

L33 ANSWER 13 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:330891 BIOSIS
DN PREV199800330891
TI Use of differential display and **DNA array** technology to assess the effect of human cytomegalovirus infection on signal transduction pathway.
AU Zhu, Hua (1); Cong, Jiang-Ping (1); Mamtora, Gargi; **Gingeras, Thomas**; Shenk, Thomas (1)

CS (1) Dep. Mol. Biol., Howard Hughes Med. Inst., Princeton Univ., Princeton, NJ 08540 USA
SO FASEB Journal, (April 24, 1998) Vol. 12, No. 8, pp. A1308.
Meeting Info.: Meeting of the American Society for Biochemistry and Molecular Biology Washington, D.C., USA May 16-20, 1998 American Society for Biochemistry and Molecular Biology
. ISSN: 0892-6638.
DT Conference
LA English
CC Medical and Clinical Microbiology - Virology *36006
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Herpesviridae 02612
Hominidae 86215
IT Major Concepts
Infection; Molecular **Genetics** (Biochemistry and Molecular Biophysics)
IT Parts, Structures, & Systems of Organisms
fibroblast
IT Diseases
human cytomegalovirus infection: viral disease
IT Chemicals & Biochemicals
interferon; mRNA [messenger RNA]: analysis
IT Methods & Equipment
differential display: analytical method; **DNA array** technology: analytical method
IT Miscellaneous Descriptors
signal transduction; Meeting Abstract
ORGN Super Taxa
Herpesviridae: Animal Viruses, Viruses, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): host; human cytomegalovirus (Herpesviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L33 ANSWER 14 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:271009 BIOSIS
DN PREV199800271009
TI Simultaneous genotyping and species identification using **hybridization** pattern recognition analysis of generic Mycobacterium **DNA arrays**.
AU **Gingeras, Thomas R. (1)**; Ghandour, Ghassan; Wang, Eugene; Berno, Anthony; Small, Peter M.; Drobniewski, Francis; Alland, David; Desmond, Edward; Holodny, Mark; Drenkow, Jorg
CS (1) Affymetrix, Santa Clara, CA 95051 USA
SO Genome Research, (May, 1998) Vol. 8, No. 5, pp. 435-448.
ISSN: 1088-9051.
DT Article
LA English
AB High-**density oligonucleotide arrays** can be used to rapidly examine large amounts of **DNA** sequence in a high throughput manner. An **array** designed to determine the specific nucleotide sequence of 705 bp of the rpoB **gene** of Mycobacterium tuberculosis accurately detected rifampin resistance associated with **mutations** of 44 clinical isolates of M. tuberculosis. The nucleotide sequence diversity in 121 Mycobacterial isolates (comprised of 10 species) was examined by both conventional dideoxynucleotide sequencing of the rpoB and 16S **genes** and by analysis of the rpoB

oligonucleotide array hybridization patterns.
Species identification for each of the isolates was similar irrespective of whether 16S sequence, rpoB sequence, or the pattern of rpoB **hybridization** was used. However for several species, the number of alleles in the 16S and rpoB **gene** sequences provided discordant estimates of the **genetic** diversity within a species. In addition to confirming the **array**'s intended utility for sequencing the region of M. tuberculosis that confers rifampin resistance, this work demonstrates that this **array** can identify the species of nontuberculous Mycobacteria. This demonstrates the general point that **DNA microarrays** that sequence important **genomic** regions (such as drug resistance or pathogenicity islands) can simultaneously identify species and provide some insight into the organism's population structure.
CC Genetics of Bacteria and Viruses *31500
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Enzymes - Methods *10804
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
BC Mycobacteriaceae 08881
IT Major Concepts
Molecular **Genetics** (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
rpoB **gene**; **DNA**: analysis
IT Methods & Equipment
hybridization pattern recognition analysis: analysis/characterization techniques, analytical method; PCR [polymerase chain reaction]: amplification method, amplification techniques, sequencing techniques, sequencing method
IT Miscellaneous Descriptors
genotyping; nucleotide sequence; species identification
ORGN Organism Name
Mycobacterium-avium; Mycobacterium-chelonae; Mycobacterium-fortuitum; Mycobacterium-gordonae; Mycobacterium-intracellulare; Mycobacterium-kansasii; Mycobacterium-scrofulaceum; Mycobacterium-smegmatis; Mycobacterium-tuberculosis; Mycobacterium-xenopi

L33 ANSWER 15 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:112588 BIOSIS
DN PREV199800112588
TI Simultaneous detection of rifampin conferring **mutations** and speciation of clinical isolates Mycobacterium using high **density oligonucleotide arrays**.
AU **Gingeras, T. R. (1)**; Small, P.; Holodniy, M.; Drenkow, J.
CS (1) Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051 USA
SO Abstracts of the Interscience Conference on Antimicrobial Agents and Chemotherapy, (1997) Vol. 37, pp. 47.
Meeting Info.: 37th Interscience Conference on Antimicrobial Agents and Chemotherapy Toronto, Ontario, Canada September 28-October 1, 1997 ICAAC .
DT Conference
LA English
CC Genetics of Bacteria and Viruses *31500
Biochemical Studies - General *10060
Bacteriology, General and Systematic *30000
Chemotherapy - General; Methods; Metabolism *38502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Mycobacteriaceae 08881
IT Major Concepts
Bacteriology; **Genetics**
IT Chemicals & Biochemicals
rifampin: antibacterial - drug; rpoB **gene**: analysis
IT Methods & Equipment
high **density oligonucleotide array**:

analytical method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Poster
ORGN Super Taxa
Mycobacteriaceae: Mycobacteria, Actinomycetes and Related Organisms, Eubacteria, Bacteria, Microorganisms
ORGN Organism Name
Mycobacterium (Mycobacteriaceae): clinical isolates; Mycobacterium-tuberculosis (Mycobacteriaceae)
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms
RN 13292-46-1 (RIFAMPIN)

L33 ANSWER 16 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:403502 BIOSIS
DN PREV199699125858
TI HIV-1 **GeneChip** and dideoxynucleotide sequence analysis of HIV-1 **genomes** present in plasma samples from patients of ACTG 143 study.
AU Mamtora, Gargi (1); Winters, M.; Drenkow, J.; Shafer, R.; Shen, N.; Tran, H.; Merigan, T.; **Gingeras, T.**
CS (1) Affymetrix, 3380 Central Expressway, Santa Clara, CA USA
SO ELEVENTH INTERNATIONAL CONFERENCE ON AIDS.. (1996) pp. 221. Eleventh International Conference on AIDS, Vol. One. One world: One hope. Publisher: Eleventh International Conference on AIDS Vancouver, British Columbia, Canada.
Meeting Info.: Eleventh International Conference on AIDS, Vol. One. One world: One hope Vancouver, British Columbia, Canada July 7-12, 1996
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
Genetics of Bacteria and Viruses *31500
Virology - Animal Host Viruses *33506
Medical and Clinical Microbiology - Virology *36006
BC Retroviridae 02623
Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Blood and Lymphatics (Transport and Circulation); **Genetics**; Infection; Methods and Techniques; Microbiology
IT Chemicals & Biochemicals
PROTEASE
IT Miscellaneous Descriptors
ANALYTICAL METHOD COMPARISON; GENOTYPING; HIGH **DENSITY OLIGONUCLEOTIDE ARRAY**; MEETING ABSTRACT; PROTEASE **GENE**; RESISTANCE-CONFERRING **GENE MUTATION**; REVERSE **TRANSCRIPTASE GENE**
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Viruses
ORGN Organism Name
human (Hominidae); human immunodeficiency virus type 1 (Retroviridae)
ORGN Organism Superterms
animals; chordates; humans; mammals; microorganisms; primates; vertebrates; viruses
RN 9001-92-7 (PROTEASE)

L33 ANSWER 17 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:400629 BIOSIS

DN PREV199699122985
TI Detection of rifampin conferring **mutations** and mycobacteria speciation using Myco **GeneChip**.
AU **Gingeras, Thomas R. (1)**; Berno, A.; Chee, M.; Drenkow, J.
CS (1) Affymetrix, 3380 Central Expressway, Santa Clara, CA USA
SO ELEVENTH INTERNATIONAL CONFERENCE ON AIDS.. (1996) pp. 218-219. Eleventh International Conference on AIDS, Vol. Two. One world: One hope. Publisher: Eleventh International Conference on AIDS Vancouver, British Columbia, Canada.
Meeting Info.: Eleventh International Conference on AIDS, Vol. Two. One world: One hope Vancouver, British Columbia, Canada July 7-12, 1996
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Physiology and Biochemistry of Bacteria *31000
Genetics of Bacteria and Viruses *31500
Medical and Clinical Microbiology - Virology *36006
Chemotherapy - Antibacterial Agents *38504
BC Mycobacteriaceae 08881
Hominidae *86215
IT Major Concepts
Genetics; Infection; Pharmacology; Physiology
IT Chemicals & Biochemicals
RIFAMPIN
IT Miscellaneous Descriptors
BACTERIAL **GENE MUTATION**; BACTERIAL IDENTIFICATION; **GENETICS**; HIGH **DENSITY OLIGONUCLEOTIDE ARRAY** ASSAY; HIV-1 INFECTION; HUMAN IMMUNODEFICIENCY VIRUS TYPE-1 INFECTION; INFECTION; MEETING ABSTRACT; METHODS AND TECHNIQUES; MYCO **GENECHIP** ASSAY; PATIENT; RIFAMPIN RESISTANCE; VIRAL DISEASE
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Mycobacteriaceae: Eubacteria, Bacteria
ORGN Organism Name
human (Hominidae); Mycobacterium spp. (Mycobacteriaceae)
ORGN Organism Superterms
animals; bacteria; chordates; eubacteria; humans; mammals; microorganisms; primates; vertebrates
RN 13292-46-1 (RIFAMPIN)

L33 ANSWER 18 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:382253 BIOSIS
DN PREV199699104609
TI Extensive polymorphisms observed in HIV-1 clade B protease **gene** using high-**density oligonucleotide arrays**.
AU Kozal, Michael J.; Shah, Nila; Shen, Naiping; Yang, Robert; Fucini, Raymond; Merigan, Thomas C.; Richman, Douglas D.; Morris, Don; Hubbell, Earl; Chee, Mark; **Gingeras, Thomas R. (1)**
CS (1) Dep. Molecular Biol., Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051 USA
SO Nature Medicine, (1996) Vol. 2, No. 7, pp. 753-759.
ISSN: 1078-8956.
DT Article
LA English
AB Naturally occurring **mutations** in HIV-1-infected patients have important implications for therapy and the outcome of clinical studies. However, little is known about the prevalence of **mutations** that confer resistance to HIV-1 protease inhibitors in isolates derived from patients naive for such inhibitors. In the first clinical application of high-**density oligonucleotide array** sequencing, the sequences of 167 viral isolates from 102 patients have been determined. The **DNA** sequence of USA HIV-1 clade B proteases was found to be extremely variable and 47.5% of the 99 amino acid positions varied. This level of amino acid diversity is greater than that

previously known for all worldwide HIV-1 clades combined (40%). Many of the amino acid changes that are known to contribute to drug resistance occurred as natural polymorphisms in isolates from patients who had never received protease inhibitors.

CC Biochemical Studies - General 10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Enzymes - Physiological Studies *10808
Pathology, General and Miscellaneous - Therapy *12512
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
Blood, Blood-Forming Organs and Body Fluids - Blood, Lymphatic and Reticuloendothelial Pathologies *15006
Blood, Blood-Forming Organs and Body Fluids - Lymphatic Tissue and Reticuloendothelial System *15008
Pharmacology - Clinical Pharmacology *22005
Genetics of Bacteria and Viruses *31500
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34508
Medical and Clinical Microbiology - Virology *36006
Chemotherapy - Antiviral Agents *38506

BC Retroviridae 02623
Hominidae *86215

IT Major Concepts
Blood and Lymphatics (Transport and Circulation); Clinical Immunology (Human Medicine, Medical Sciences); Enzymology (Biochemistry and Molecular Biophysics); **Genetics**; Hematology (Human Medicine, Medical Sciences); Infection; Pathology; Pharmacology

IT Chemicals & Biochemicals
PROTEASE; PROTEASE INHIBITOR

IT Sequence Data
dna sequence

IT Miscellaneous Descriptors
AMINO ACID DIVERSITY; DRUG RESISTANCE; PROTEASE INHIBITOR THERAPY

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Viruses

ORGN Organism Name
human (Hominidae); human immunodeficiency virus-1 (Retroviridae)

ORGN Organism Superterms
animals; chordates; humans; mammals; microorganisms; primates; vertebrates; viruses

RN 9001-92-7 (PROTEASE)
37205-61-1 (PROTEASE INHIBITOR)

L33 ANSWER 19 OF 19 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1987:456842 BIOSIS
DN BR33:105413
TI COVALENT ATTACHMENT OF **NUCLEIC ACIDS** TO **SOLID SUPPORTS CHEMISTRIES** OF COUPLING AND **HYBRIDIZATION** CHARACTERISTICS.
AU GHOSH S S; **GINGERAS T R**; DAVIS G R; MUSSO G F; KWOH D Y; KAO P M
CS SALK INST. BIOTECHNOL./IND. ASSOC. INC., P.O. BOX 85200, LA JOLLA, CALIF. 92037, USA.
SO 194TH AMERICAN CHEMICAL SOCIETY NATIONAL MEETING, NEW ORLEANS, LOUISIANA, USA, AUGUST 30-SEPTEMBER 4, 1987. ABSTR PAP AM CHEM SOC. (1987) 194 (0), MBTD 68.
CODEN: ACSRAL. ISSN: 0065-7727.
DT Conference
FS BR; OLD
LA English

CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General 03502
Comparative Biochemistry, General 10010
Biochemical Methods - General 10050

Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biophysics - Molecular Properties and Macromolecules 10506
Biophysics - Bioengineering *10511
IT Miscellaneous Descriptors
ABSTRACT BIOTECHNOLOGY NON-SPECIFIC BONDING

=> d all tot

L38 ANSWER 1 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:49474 BIOSIS
DN PREV200100049474
TI Beyond the Human Genome.
AU Ezzell, Carol
SO Scientific American, (July, 2000) Vol. 283, No. 1, pp. 64-69. print.
ISSN: 0036-8733.
DT Article
LA English
SL English
CC Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
protein: expression, identification
IT Methods & Equipment
DNA sequencing: sequencing method, sequencing techniques;
GeneChip System: equipment; protein chip: equipment
IT Miscellaneous Descriptors
Human Genome Project
CO **Affymetrix: company/organization;** Celera Genomics: company/organization; Ciphergen Biosystems: company/organization; Human Genome Sciences: company/organization; National Cancer Institute: company/organization; National Institute of Health: company/organization
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 2 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:28219 BIOSIS
DN PREV200100028219
TI Identification of IEX-1, a mechanically induced apoptosis regulatory gene, in cardiac myocytes through DNA microarray technology.
AU De Keulenaer, Gilles W. (1); Landschulz, Katherine T.; Turi, Thomas G.; Thompson, John F.; Dang, Quynh; Lee, Richard T.
CS (1) Brigham and Women's Hosp, Boston, MA USA
SO Circulation, (October 31, 2000) Vol. 102, No. 18 Supplement, pp. II.213. print.
Meeting Info.: Abstracts from Scientific Sessions 2000 New Orleans, Louisiana, USA November 12-15, 2000
ISSN: 0009-7322.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - General *03502
General Biology - Symposia, Transactions and Proceedings of Conferences,

Congresses, Review Annuals *00520
Cytology and Cytochemistry - Animal *02506
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Cardiovascular System - Physiology and Biochemistry *14504
Muscle - Physiology and Biochemistry *17504
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Cardiovascular System (Transport and Circulation)
IT Parts, Structures, & Systems of Organisms
cardiac myocytes: circulatory system, cultured, muscular system; left ventricle: circulatory system; right ventricle: circulatory system
IT Chemicals & Biochemicals
IEX-2 mRNA: expression
IT Methods & Equipment
Affymetrix GeneChip System: equipment; DNA microarray: analytical method; Northern blot: Recombinant DNA Technology, analytical method, detection/labeling techniques, gene mapping, molecular probe techniques
IT Miscellaneous Descriptors
apoptosis; biomechanical stress; Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
rat (Muridae)
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L38 ANSWER 3 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:538836 BIOSIS
DN PREV200000538836
TI Cancer research applications using **Affymetrix** high density **genechip** probe arrays.
AU Haase, B. (1)
CS (1) **Affymetrix** UK Ltd., Oxon UK
SO Tumor Biology, (September, 2000) Vol. 21, No. Supplement 1, pp. 3. print.
Meeting Info.: 28th Meeting of the International Society for Oncodevelopmental Biology and Medicine Munich, Germany September 08-13, 2000
ISSN: 1010-4283.
DT Conference
LA English
SL English
CC Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Blood, Blood-Forming Organs and Body Fluids - Blood, Lymphatic and Reticuloendothelial Pathologies *15006
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Blood and Reticuloendothelial Neoplasms *24010
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Oncology (Human Medicine, Medical Sciences); Methods and Techniques
IT Diseases
acute leukemia: blood and lymphatic disease, neoplastic disease; cancer: classification, neoplastic disease
IT Chemicals & Biochemicals
DNA: sequences, variations; RNA: variations; gene: expression-monitoring, function, regulation
IT Alternate Indexing
Leukemia (MeSH); Neoplasms (MeSH)
IT Methods & Equipment
Affymetrix high density **genechip** probe: laboratory equipment

IT Miscellaneous Descriptors
cancer research: applications; Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 4 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:524857 BIOSIS
DN PREV200000524857
TI Differential gene expression profiles due to lithium and bipolar disorder.
AU Ebstein, R. P. (1); Horn-Saban, S.; Nemanov, L. (1); Shamir, A.; Belmaker, R. H.; Agam, G.
CS (1) Herzog Hospital, Jerusalem, 9135 Israel
SO American Journal of Medical Genetics, (August 7, 2000) Vol. 96, No. 4, pp. 482. print.
Meeting Info.: Eighth World Congress on Psychiatric Genetics Versailles, France August 27-31, 2000 International Society of Psychiatric Genetics . ISSN: 0148-7299.
DT Conference
LA English
SL English
CC Pharmacology - Psychopharmacology *22026
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Behavioral Biology - General and Comparative Behavior *07002
Behavioral Biology - Human Behavior *07004
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Minerals *10069
Pathology, General and Miscellaneous - Therapy *12512
Psychiatry - Psychopathology; Psychodynamics and Therapy *21002
Pharmacology - General *22002
Pharmacology - Clinical Pharmacology *22005
IT Major Concepts
Behavior; Molecular Genetics (Biochemistry and Molecular Biophysics); Pharmacology
IT Diseases
bipolar disorder: behavioral and mental disorders
IT Chemicals & Biochemicals
lithium: antipsychotic - drug; messenger RNA: expression
IT Alternate Indexing
Bipolar Disorder (MeSH)
IT Methods & Equipment
Affymetrix GeneChip probe array: genetic analytical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 7439-93-2 (LITHIUM)

L38 ANSWER 5 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:524837 BIOSIS
DN PREV200000524837
TI Evaluation of the performance of a p53 sequencing microarray chip using 140 previously sequenced bladder tumor samples.
AU Wikman, Friedrik P.; Lu, Ming-Lan; Thykjaer, Thomas; Olesen, Sanne H.; Andersen, Lars D.; Cordon-Cardo, Carlos; Orntoft, Torben F. (1)

CS (1) Department of Clinical Biochemistry, Skejby Sygehus, Brendstrupgaardsvej, 8200, Aarhus N Denmark
SO Clinical Chemistry, (October, 2000) Vol. 46, No. 10, pp. 1555-1561. print. ISSN: 0009-9147.
DT Article
LA English
SL English
AB Background: Testing for mutations of the TP53 gene in tumors is a valuable predictor for disease outcome in certain cancers, but the time and cost of conventional sequencing limit its use. The present study compares traditional sequencing with the much faster microarray sequencing on a commercially available chip and describes a method to increase the specificity of the chip. Methods: DNA from 140 human bladder tumors was extracted and subjected to a multiplex-PCR before loading onto the p53 **GeneChip** from **Affymetrix**. The same samples were previously sequenced by manual dideoxy sequencing. In addition, two cell lines with two different homozygous mutations at the TP53 gene locus were analyzed. Results: Of 1464 gene chip positions, each of which corresponded to an analyzed nucleotide in the sequence, 251 had background signals that were not attributable to mutations, causing the specificity of mutation calling without mathematical correction to be low. This problem was solved by regarding each chip position as a separate entity with its own noise and threshold characteristics. The use of background plus 2 SD as the cutoff improved the specificity from 0.34 to 0.86 at the cost of a reduced sensitivity, from 0.92 to 0.84, leading to a much better concordance (92%) with results obtained by traditional sequencing. The chip method detected as little as 1% mutated DNA. Conclusions: Microarray-based sequencing is a novel option to assess TP53 mutations, representing a fast and inexpensive method compared with conventional sequencing.
CC Genetics and Cytogenetics - Human *03508
General Biology - Information, Documentation, Retrieval and Computer Applications *00530
Genetics and Cytogenetics - General *03502
Urinary System and External Secretions - Pathology *15506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Computer Applications (Computational Biology); Urology (Human Medicine, Medical Sciences)
IT Diseases
bladder tumor: neoplastic disease, urologic disease
IT Chemicals & Biochemicals
human TP53 gene (Hominidae): mutations
IT Alternate Indexing
Bladder Neoplasms (MeSH)
IT Methods & Equipment
microarray sequencing: sequencing method; p53 **GeneChip**: **Affymetrix**; p53 sequencing microarray chip
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 6 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:452586 BIOSIS
DN PREV200000452586
TI From DNA biosensors to gene chips.
AU Wang, Joseph (1)
CS (1) Department of Chemistry and Biochemistry, New Mexico State University, Las Cruces, NM, 88003 USA
SO Nucleic Acids Research, (August 15, 2000) Vol. 28, No. 16, pp. 3011-3016. print.
ISSN: 0305-1048.

DT Article
LA English
SL English
AB Wide-scale DNA testing requires the development of small, fast and easy-to-use devices. This article describes the preparation, operation and applications of biosensors and gene chips, which provide fast, sensitive and selective detection of DNA hybridization. Various new strategies for DNA biosensors and gene chips are examined, along with recent trends and future directions. The integration of hybridization detection schemes with the sample preparation process in a 'Lab-on-a-Chip' format is also covered. While the use of DNA biosensors and gene chips is at an early stage, such devices are expected to have an enormous effect on future DNA diagnostics.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Chemicals & Biochemicals
DNA
IT Methods & Equipment
Affymetrix GeneChip: Affymetrix, equipment; DNA biosensor: equipment; DNA hybridization: detection method, detection/labeling techniques; microarray analysis: genetic analysis, genetic method
IT Miscellaneous Descriptors
gene chips

L38 ANSWER 7 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:445476 BIOSIS
DN PREV200000445476
TI Direct comparison of **GeneChip** and SAGE on the quantitative accuracy in transcript profiling analysis.
AU Ishii, Masami; Hashimoto, Shin-ichi; Tsutsumi, Shuichi; Wada, Yoichiro; Matsushima, Kouji; Kodama, Tatsuhiko; Aburatani, Hiroyuki (1)
CS (1) RCAST No. 20, University of Tokyo, 4-6-1 Komaba Meguro-ku, Tokyo, 153-8904 Japan
SO Genomics, (September 1, 2000) Vol. 68, No. 2, pp. 136-143. print.
ISSN: 0888-7543.
DT Article
LA English
SL English
AB Among the high-throughput, comprehensive technological methods used to analyze transcript expression levels, array-based hybridization and serial analysis of gene expression (SAGE) are currently the most common approaches. To compare the quantitative accuracy of oligonucleotide array and SAGE, both methods were carried out on identical RNA specimens prepared from human blood monocytes and granulocyte-macrophage colony-stimulating factor (GM-CSF)-induced macrophages. For SAGE analysis, 57,560 and 57,463 tags were obtained from monocytes and macrophages, respectively, resulting in approximately 28,000 different tags, while oligo array hybridization was performed with **GeneChip** (**Affymetrix**), which represents approximately 6000 transcripts. These two methods correlated quite well in both absolute expression analyses and comparative analyses during differentiation. The correlation was better for genes with higher expression levels and greater changes in expression. This finding suggests that **GeneChip** technology is reasonably reliable for quantitative analysis of expression profiling and would be appropriate as a common platform upon which to build a gene expression database.
CC Immunology and Immunochemistry - General; Methods *34502
Cytology and Cytochemistry - Animal *02506
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062

Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
Endocrine System - General *17002
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Parts, Structures, & Systems of Organisms
macrophages: blood and lymphatics, immune system; monocytes: blood and lymphatics, immune system
IT Chemicals & Biochemicals
RNA; granulocyte-macrophage colony-stimulating factor
IT Methods & Equipment
GeneChip: analytical method; oligonucleotide array: analytical method; serial analysis of gene expression: analytical method; transcript profiling analysis: analytical method
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 83869-56-1 (GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR)

L38 ANSWER 8 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:442717 BIOSIS
DN PREV200000442717
TI The effect of high-glucose on total gene expression in human islets measured by **Affymetrix** GeneChipTM arrays.
AU Johnson, J. D. (1); Palma, J. F.; Moldover, B.; Guo, J.; Korbutt, G.; Blume, J.
CS (1) Dept. of Genomics, Metabolex, Inc., 3876 Bay Center Place, Hayward, CA, 94545 USA
SO Diabetologia, (August, 2000) Vol. 43, No. Supplement 1, pp. A57. print. Meeting Info.: 36th Annual Meeting of the European Association for the Study of Diabetes Jerusalem, Israel September 17-21, 2000 European Association for the Study of Diabetes
. ISSN: 0012-186X.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Biochemical Studies - Carbohydrates *10068
Enzymes - General and Comparative Studies; Coenzymes *10802
Metabolism - General Metabolism; Metabolic Pathways *13002
Endocrine System - General *17002
IT Major Concepts
Medical Genetics (Allied Medical Sciences); Equipment, Apparatus, Devices and Instrumentation; Clinical Endocrinology (Human Medicine, Medical Sciences); Metabolism
IT Parts, Structures, & Systems of Organisms
complex nutritional conditions: endocrine system
IT Chemicals & Biochemicals
glucose; insulin messenger RNA; islet-amyloid polypeptide; islet-amyloid propeptide messenger RNA; pancreatic islet genes: expression; prohormone convertase; prohormone convertase messenger RNA; proinsulin convertase; proinsulin convertase messenger RNA; islet amyloid polypeptide gene (Hominidae): expression; prohormone convertase gene (Hominidae): expression; proinsulin convertase gene (Hominidae): expression
IT Methods & Equipment
Affymetrix GeneChip arrays: medical equipment
IT Miscellaneous Descriptors

Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 50-99-7Q (GLUCOSE)
58367-01-4Q (GLUCOSE)
106602-62-4 (ISLET-AMYLOID POLYPEPTIDE)
99676-46-7 (PROHORMONE CONVERTASE)

L38 ANSWER 9 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:439654 BIOSIS
DN PREV200000439654
TI From genome-wide expression analysis in cancer to novel targets for antibody therapeutics.
AU Murray, Richard
SO Acta Haematologica (Basel), (July, 2000) Vol. 103, No. Supplement 1, pp. 90. print.
Meeting Info.: 13th Symposium on Molecular Biology of Hematopoiesis and Treatment of Leukemia and Cancer New York, NY, USA July 14-18, 2000
ISSN: 0001-5792.
DT Conference
LA English
SL English
CC Immunology and Immunochemistry - General; Methods *34502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques; Tumor Biology
IT Diseases
breast cancer: neoplastic disease, reproductive system disease/female
IT Chemicals & Biochemicals
antibodies: therapeutic
IT Alternate Indexing
Breast Neoplasms (MeSH)
IT Methods & Equipment
Affymetrix GeneChip microarray: analytical method; gene cloning: cloning method; genome-wide expression analysis: analytical method; in situ hybridization: analytical method; tumor tissue assay: analytical method
IT Miscellaneous Descriptors
gene expression database; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 10 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:421424 BIOSIS
DN PREV200000421424
TI Comparative evaluation of three human immunodeficiency virus genotyping systems: The HIV-GenotypR method, the HIV PRT **GeneChip** assay, and the HIV-1 RT Line Probe Assay.
AU Wilson, John W. (1); Bean, Pamela; Robins, Terry; Graziano, Frank; Persing, David H.

CS (1) Division of Infectious Diseases, Mayo Clinic, 200 First St., SW, Rochester, MN, 55905 USA
SO Journal of Clinical Microbiology, (August, 2000) Vol. 38, No. 8, pp. 3022-3028. print.
ISSN: 0095-1137.
DT Article
LA English
SL English
AB Evaluation of drug resistance by human immunodeficiency virus (HIV) genotyping has proven to be useful for the selection of drug combinations with maximum antiretroviral activity. We compared three genotyping methods for identification of mutations known to confer drug resistance in the reverse transcriptase (RT) and protease genes of HIV type 1 (HIV-1). The HIV-GenotypR method (GenotypR; Specialty Laboratories, Inc., Santa Monica, Calif.) with the ABI 377 DNA sequencer (Applied Biosystems Inc.), the HIV PRT **GeneChip** assay (**GeneChip**; **Affymetrix**, Santa Clara, Calif.), and the HIV-1 RT Line Probe Assay (LiPA; Innogenetics, Alpharetta, Ga.) were used to genotype plasma samples from HIV-infected patients attending the University of Wisconsin Hospitals and Clinics and the Mayo Clinic. At the time of analysis, patients were failing combination therapy (n = 18) or were treatment naive (n = 6). Forty codons of the RT and protease genes were analyzed by GenotypR and **GeneChip** for resistance-associated mutations. LiPA analyzed seven RT codons for mutations. Each sample was genotyped by all three assays, and each assay was subjected to pairwise comparisons. At least 92% of the codons tested (by the three assays) in paired comparisons were concordant. GenotypR and **GeneChip** demonstrated 96.6% concordance over the 40 codons tested. GenotypR identified slightly more mutations than **GeneChip** and LiPA; **GeneChip** identified all primary mutations that corresponded to failing treatment regimens. Each assay identified at least 84% of the mutations identified by the other assays. Mutations that were discordant between the assays mainly comprised secondary mutations and natural polymorphisms. The assays had better concordance for mutations that corresponded to current failing regimens, present in the more predominant viral quasispecies. In the treatment-naive patients, GenotypR, **GeneChip**, and LiPA mainly identified wild-type virus. Only the LiPA identified K70R, a possible transmitted zidovudine resistance mutation, in the RT gene of a treatment-naive patient. We conclude that although discrepancies in results exist between assays, each assay showed a similar capacity to identify potentially clinically relevant mutations related to patient treatment regimens.
CC Genetics and Cytogenetics - Human *03508
Genetics and Cytogenetics - General *03502
Pathology, General and Miscellaneous - Therapy *12512
Pharmacology - General *22002
Pharmacology - Clinical Pharmacology *22005
Genetics of Bacteria and Viruses *31500
Virology - Animal Host Viruses *33506
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34508
Medical and Clinical Microbiology - Virology *36006
BC Retroviridae 02623
IT Major Concepts
Genetics; Infection; Methods and Techniques; Pharmacology
IT Diseases
human immunodeficiency virus infection [HIV infection]: immune system disease, viral disease
IT Alternate Indexing
HIV Infections (MeSH)
IT Methods & Equipment
HIV PRT **GeneChip** assay: genetic method, identification method; HIV-1 RT Line Probe assay: genetic method, identification method; HIV-GenotypR method: genetic method, identification method
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Animal Viruses, Viruses, Microorganisms

ORGN Organism Name
human (Hominidae): patient; human immunodeficiency virus [HIV] (Retroviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L38 ANSWER 11 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:337293 BIOSIS
DN PREV200000337293
TI Technical assessment of the **Affymetrix** yeast expression **GeneChip** YE6100 platform in a heterologous model of genes that confer resistance to antimalarial drugs in yeast.
AU Nau, Martin E.; Emerson, Lyndal R.; Martin, Rodger K.; Kyle, Dennis E.; Wirth, Dyann F.; Vahey, Maryanne (1)
CS (1) Gene Array Laboratory, Walter Reed Army Institute of Research, 1600 East Gude Dr., Rockville, MD, 20850 USA
SO Journal of Clinical Microbiology, (May, 2000) Vol. 38, No. 5, pp. 1901-1908. print.
ISSN: 0095-1137.
DT Article
LA English
SL English
AB The advent of high-density gene array technology has revolutionized approaches to drug design, development, and characterization. At the laboratory level, the efficient, consistent, and dependable exploitation of this complex technology requires the stringent standardization of protocols and data analysis platforms. The **Affymetrix** YE6100 expression **GeneChip** platform was evaluated for its performance in the analysis of both global (6,000 yeast genes) and targeted (three pleiotropic multidrug resistance genes of the ATP binding cassette transporter family) gene expression in a heterologous yeast model system in the presence and absence of the antimalarial drug chloroquine. Critical to the generation of consistent data from this platform are issues involving the preparation of the specimen, use of appropriate controls, accurate assessment of experiment variance, strict adherence to optimized enzymatic and hybridization protocols, and use of sophisticated bioinformatics tools for data analysis.
CC Genetics and Cytogenetics - Plant *03504
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
Medical and Clinical Microbiology - Mycology *36008
Chemotherapy - Antiparasitic Agents *38510
IT Major Concepts
Genetics; Methods and Techniques; Pharmacology
IT Chemicals & Biochemicals
chloroquine: antiparasitic - drug
IT Methods & Equipment
Affymetrix Yeast Expression **GeneChip** YE6100 Platform: analytical method, genetic method, technical assessment
ORGN Super Taxa
Ascomycetes: Fungi, Plantae
ORGN Organism Name
Saccharomyces cerevisiae (Ascomycetes): pathogen
ORGN Organism Superterms
Fungi; Microorganisms; Nonvascular Plants; Plants
RN 54-05-7 (CHLOROQUINE)

L38 ANSWER 12 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:243314 BIOSIS
DN PREV200000243314
TI Using **Genechip** technology to examine global gene expression in human disease.
AU Harrington, Christina A. (1); Dieckgraefe, Brian
CS (1) **Affymetrix**, Inc., Santa Clara, CA USA
SO Pfluegers Archiv European Journal of Physiology, (2000) Vol. 439, No. 3

Suppl., pp. R68.
Meeting Info.: 1998 Life Sciences Conference: Signalling Concepts in Life Sciences. Godz Martuljek, Slovenia September 19-24, 1998
ISSN: 0031-6768.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
Pathology, General and Miscellaneous - Inflammation and Inflammatory Disease *12508
Metabolism - General Metabolism; Metabolic Pathways *13002
Digestive System - General; Methods *14001
Pathology, General and Miscellaneous - Therapy *12512
Pathology, General and Miscellaneous - Diagnostic *12504
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Genetics; Gastroenterology (Human Medicine, Medical Sciences); Methods and Techniques
IT Diseases
Crohn's disease: digestive system disease, immune system disease; inflammatory bowel disease: digestive system disease; ulcerative colitis: digestive system disease
IT Chemicals & Biochemicals
RNA; mRNA [messenger RNA]
IT Alternate Indexing
Crohn Disease (MeSH); Inflammatory Bowel Diseases (MeSH); Colitis, Ulcerative (MeSH)
IT Methods & Equipment
Genechip expression analysis: genetic method
IT Miscellaneous Descriptors
gene expression; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 13 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:234176 BIOSIS
DN PREV200000234176
TI Monitoring of expression of genes using high-density oligonucleotide DNA array (GeneChipTM, **Affymetrix**) during ischemia-reperfusion in mouse hippocampus.
AU Nagata, Toshihito (1); Asai, Satoshi (1); Takahashi, Yasuo (1); Zhao, Heng (1); Ishikawa, Koichi (1)
CS (1) Department of Pharmacology, Nihon University, School of Medicine, 30 Oyaguchi Kami-machi, Itabashi-ku, Tokyo, 173-0032 Japan
SO Japanese Journal of Pharmacology, (2000) Vol. 82, No. Suppl. 1, pp. 106P.
Meeting Info.: 73rd Annual Meeting of the Japanese Pharmacological Society. Yokohama, Japan March 23-25, 2000
ISSN: 0021-5198.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Animal *03506
Cardiovascular System - Blood Vessel Pathology *14508
Nervous System - Physiology and Biochemistry *20504
Pharmacology - General *22002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Genetics; Methods and Techniques; Nervous System (Neural Coordination);

Pharmacology
IT Parts, Structures, & Systems of Organisms
hippocampus: nervous system; neuronal cells: nervous system
IT Diseases
ischemia-reperfusion: vascular disease
IT Alternate Indexing
Reperfusion Injury (MeSH)
IT Methods & Equipment
high-density oligonucleotide DNA array [**Affymetrix**, **GeneChip**]: analytical method
IT Miscellaneous Descriptors
gene expression monitoring; Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae)
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L38 ANSWER 14 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:148106 BIOSIS
DN PREV200000148106
TI Use of **GeneChip**(R) microarrays to identify the spectrum of transcriptional changes associated with differentiation of a neural cell line.
AU Harrington, C. A. (1); Venkatapathy, S. (1); Wood, I.; Buckley, N.
CS (1) **Affymetrix**, Inc., Santa Clara, CA, 95051 USA
SO Society for Neuroscience Abstracts., (1999) Vol. 25, No. 1-2, pp. 2042. Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999 Society for Neuroscience . ISSN: 0190-5295.
DT Conference
LA English
SL English
CC Nervous System - General; Methods *20501
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Developmental Biology - Embryology - General and Descriptive *25502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques; Nervous System (Neural Coordination)
IT Chemicals & Biochemicals
neural-specific marker genes: expression
IT Methods & Equipment
GeneChip microarrays: analytical method, genetic method
IT Miscellaneous Descriptors
gene expression; neuronal differentiation; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
NBOK-1 cell line (Hominidae): neuroblastoma cell; human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 15 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:146019 BIOSIS
DN PREV200000146019
TI Developmental profiling of hippocampal gene expression using the GeneChipTM technology.
AU Cao, Y. (1); Mody, M.; Shimizu, E.; Lockhart, D. J. (1); Tsien, J. Z.
CS (1) **Affymetrix** Inc., 3380 Central Expressway, Santa Clara, CA, 95051 USA

SO Society for Neuroscience Abstracts., (1999) Vol. 25, No. 1-2, pp. 1305.
Meeting Info.: 29th Annual Meeting of the Society for Neuroscience. Miami Beach, Florida, USA October 23-28, 1999 Society for Neuroscience
. ISSN: 0190-5295.
DT Conference
LA English
SL English
CC Nervous System - General; Methods *20501
Genetics and Cytogenetics - Animal *03506
Biochemical Studies - General *10060
Toxicology - Foods, Food Residues, Additives and Preservatives *22502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Muridae 86375
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Development; Nervous System (Neural Coordination)
IT Parts, Structures, & Systems of Organisms
hippocampus: development, nervous system
IT Chemicals & Biochemicals
mouse gene: expression, hippocampus
IT Methods & Equipment
GeneChip technology: equipment; high-density oligonucleotide array: biochemical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae): embryo, fetus, neonate
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L38 ANSWER 16 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:14670 BIOSIS
DN PREV200000014670
TI Microarray analysis of gene expression and proteomics in severe pulmonary hypertension and normal human lung.
AU Geraci, Mark W. (1); Gao, Bifeng (1); Moore, Mark D. (1); Lepley, Robert A.; Tuder, Rubin M.; Voelkel, Norbert F.
CS (1) Univ of Colorado Health Scis Ctr, Denver, CO USA
SO Circulation, (Nov. 2, 1999) Vol. 110, No. 18 SUPPL., pp. I.241.
Meeting Info.: 72nd Scientific Sessions of the American Heart Association Atlanta, Georgia, USA November 7-10, 1999
ISSN: 0009-7322.
DT Conference
LA English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Cardiovascular System - General; Methods *14501
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Cardiovascular System (Transport and Circulation)
IT Parts, Structures, & Systems of Organisms
lung: respiratory system
IT Diseases
pulmonary hypertension: vascular disease
IT Alternate Indexing
Hypertension, Pulmonary (MeSH)
IT Methods & Equipment
Affymetrix GeneChip: laboratory equipment; PAGE [polyacrylamide gel electrophoresis]: analytical method; microassay analysis: analytical method

IT Miscellaneous Descriptors
gene expression; proteomics; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L38 ANSWER 17 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:483186 BIOSIS
DN PREV199900483186
TI High-density nucleoside analog probe arrays for enhanced hybridization.
AU Fidanza, Jacqueline A. (1); McGall, Glenn H.
CS (1) **Affymetrix**, Inc., 3380 Central Expressway, Santa Clara, CA USA
SO Nucleosides & Nucleotides, (June July, 1999) Vol. 18, No. 6-7, pp. 1293-1295.
ISSN: 0732-8311.
DT Article
LA English
SL English
AB DNA probe arrays were synthesized with analogs of 2,6-diaminopurine and 2'-O-methyl-thymidine in place of A and T. AT-rich **GeneChip**(R) test arrays containing 14-mer or 20-mer analog probes improved hybridization to fluorescently-labeled RNA sequences under stringent conditions.
CC Genetics and Cytogenetics - General *03502
Biochemical Methods - General *10050
Biochemical Studies - General *10060
Biophysics - Molecular Properties and Macromolecules *10506
Genetics of Bacteria and Viruses *31500
Virology - Animal Host Viruses *33506
BC Retroviridae 02623
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA: probe, synthesis; RNA: hybridization; 2,6-diaminopurine; 2'-O-methyl-thymidine
IT Methods & Equipment
GeneChip test array: analytical method
IT Miscellaneous Descriptors
DNA analog probe array: synthesis
ORGN Super Taxa
Retroviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
HIV [human immunodeficiency virus] (Retroviridae)
ORGN Organism Superterms
Animal Viruses; Microorganisms; Viruses
RN 1904-98-9 (2,6-DIAMINOPURINE)

L38 ANSWER 18 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:413948 BIOSIS
DN PREV199900413948
TI Performance of the **Affymetrix GeneChip** HIV PRT 440 platform for antiretroviral drug resistance genotyping of human immunodeficiency virus type 1 clades and viral isolates with length polymorphisms.
AU Vahey, Maryanne (1); Nau, Martin E.; Barrick, Sandra; Cooley, John D.; Sawyer, Robert; Sleeker, Alex A.; Vickerman, Peter; Bloor, Stuart; Larder, Brendan; Michael, Nelson L.; Wegner, Scott A.
CS (1) Division of Retrovirology, Walter Reed Army Institute of Research, 1600 E. Gude Dr., Rockville, MD, 20850 USA
SO Journal of Clinical Microbiology, (Aug., 1999) Vol. 37, No. 8, pp. 2533-2537.

ISSN: 0095-1137.
DT Article
LA English
SL English
AB The performance of a silica chip-based resequencing method, the **Affymetrix** HIV PRT 440 assay (hereafter referred to as the **Affymetrix** assay), was evaluated on a panel of well-characterized nonclade B viral isolates and on isolates exhibiting length polymorphisms. Sequencing of human immunodeficiency virus type 1 (HIV-1) pol cDNAs from clades A, C, D, E, and F resulted in clade-specific regions of base-calling ambiguities in regions not known to be associated with resistance polymorphisms, as well as a small number of spurious resistance polymorphisms. The **Affymetrix** assay failed to detect the presence of additional serine codons distal to reverse transcriptase (RT) codon 68 that are associated with multinucleoside RT inhibitor resistance. The increasing prevalence of non-clade B HIV-1 strains in the United States and Europe and the identification of clinically relevant pol gene length polymorphisms will impact the generalizability of the **Affymetrix** assay, emphasizing the need to accommodate this expanding pool of pol genotypes in future assay versions.
CC Genetics of Bacteria and Viruses *31500
Clinical Biochemistry; General Methods and Applications *10006
Biochemical Studies - General *10060
Medical and Clinical Microbiology - Virology *36006
Virology - General; Methods *33502
Enzymes - General and Comparative Studies; Coenzymes *10802
BC Retroviridae 02623
Hominidae 86215
IT Major Concepts
Clinical Chemistry (Allied Medical Sciences); Infection; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Parts, Structures, & Systems of Organisms
plasma: blood and lymphatics
IT Chemicals & Biochemicals
pol cDNAs [polymerase complementary DNAs]; reverse transcriptase [RT]; human immunodeficiency virus type 1 pol gene (Retroviridae)
IT Methods & Equipment
Affymetrix GeneChip HIV PRT 440 Platform: diagnostic method, laboratory equipment, molecular genetic method, performance
IT Miscellaneous Descriptors
antiretroviral drug resistance; length polymorphisms
GT Europe (Palearctic region); USA (North America, Nearctic region)
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
human (Hominidae): host; human immunodeficiency virus type 1 [HIV-1] (Retroviridae): clade A, clade C, clade D, pathogen, clade F, clade E
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L38 ANSWER 19 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:342377 BIOSIS
DN PREV199900342377
TI Novel strategy yields candidate Gsh-1 homeobox gene targets using hypothalamus progenitor cell lines.
AU Li, Hung (1); Schrick, Jeffrey J.; Fewell, Gwen D.; MacFarland, Kevin L.; Witte, David P.; Bodenmiller, Diane M.; Hsieh-Li, H.-M. (1); Su, C.-Y. (1); Potter, S. Steven
CS (1) Institute of Molecular Biology, Academia Sinica, Taipei, Taiwan, 11529 China
SO Developmental Biology, (July 1, 1999) Vol. 211, No. 1, pp. 64-76. ISSN: 0012-1606.
DT Article

LA English
SL English
AB We describe the successful application of a strategy that potentially provides for an efficient and universal screen for downstream gene targets. We used the promoter of the Gsh-1 homeobox gene to drive expression of the SV40 T-antigen gene in transgenic mice. We have previously shown that the Gsh-1 homeobox gene is expressed in discrete domains of the ganglionic eminences, diencephalon, and hindbrain during brain development. Gsh-1-SV40 T transgenic mice showed cellular hyperplasia in regions of the brain coincident with Gsh-1 expression. The Gsh-1-SV40 T transgene was introduced, by breeding, into Gsh-1 homozygous mutant mice, and Gsh-1 -/- cell lines were made. Clonal cell lines were generated and analyzed by Northern blot hybridizations and **Affymetrix GeneChip** probe arrays to determine gene expression profiles. The results indicate that the cell lines remain representative of early developmental stages. Further, immunocytochemistry showed uniformly high levels of nestin expression,typical of central nervous system progenitor cells, and the absence of terminal differentiation markers of neuronal cells. One clonal cell line, No. 14, was then stably transfected with a tet-inducible Gsh-1 expression construct and subcloned. The starting clone 14, together with the uninduced and induced subclones, provided cell populations with varying levels of Gsh-1 expression. Differential display and **Affymetrix GeneChip** probe arrays were then used to identify transcript differences that represent candidate Gsh-1 target genes. Of particular interest, the drm and gas1 genes, which repress cell proliferation, were observed to be activated in Gsh-1-expressing cells. These observations support models predicting that homeobox genes function in the regulation of cell proliferation.
CC Genetics and Cytogenetics - Animal *03506
Cytology and Cytochemistry - Animal *02506
Nervous System - General; Methods *20501
Developmental Biology - Embryology - General and Descriptive *25502
BC Muridae 86375
IT Major Concepts
Development; Molecular Genetics (Biochemistry and Molecular Biophysics); Nervous System (Neural Coordination)
IT Parts, Structures, & Systems of Organisms
brain: development, nervous system; central nervous system: nervous system; diencephalon: nervous system; hindbrain: nervous system; hypothalamus: nervous system; progenitor cell: blood and lymphatics
IT Chemicals & Biochemicals
nestin; drm gene (Muridae); gas 1 gene (Muridae); Gsh-1 gene (Muridae); SV40 T-antigen gene (Muridae)
IT Miscellaneous Descriptors
organogenesis
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae): transgenic
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L38 ANSWER 20 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:113770 BIOSIS
DN PREV199800113770
TI High sensitivity method for HIV-1 genotyping using the **GeneChip** HIV PRT assay.
AU Hurt, M. H. (1); Miyada, C. G.; Do, D.; Ryder, T.; Kaplan, P.
CS (1) **Affymetrix** Inc., 3380 Central Expressway, Santa Clara, CA 95051 USA
SO Abstracts of the Interscience Conference on Antimicrobial Agents and Chemotherapy, (1997) Vol. 37, pp. 263.
Meeting Info.: 37th Interscience Conference on Antimicrobial Agents and Chemotherapy Toronto, Ontario, Canada September 28-October 1, 1997 ICAAC

DT Conference
LA English
CC Medical and Clinical Microbiology - Virology *36006
Pathology, General and Miscellaneous - Therapy *12512
Pharmacology - Clinical Pharmacology *22005
Genetics of Bacteria and Viruses *31500
Chemotherapy - Antiviral Agents *38506
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Retroviridae 02623
Hominidae 86215
IT Major Concepts
Methods and Techniques
IT Diseases
HIV infection: viral disease
IT Chemicals & Biochemicals
DNA; RNA
IT Methods & Equipment
antiretroviral therapy: therapeutic method; **GeneChip** HIV PRT assay: analytical method
IT Miscellaneous Descriptors
drug resistance; HIV-1 genotyping; Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
human (Hominidae): host; human immunodeficiency virus 1 (Retroviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L38 ANSWER 21 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:111415 BIOSIS
DN PREV199800111415
TI Cytochrome P450 genotyping using high density arrays of oligonucleotide probes.
AU Liu, W. W.; Webster, T.; Aggarwal, A.; Pho, M.; Cronin, M.; Ryder, T.
CS **Affymetrix** Inc., 3380 Central Expressway, Santa Clara, CA 95051 USA
SO American Journal of Human Genetics, (Oct., 1997) Vol. 61, No. 4 SUPPL., pp. A257.
Meeting Info.: 47th Annual Meeting of the American Society of Human Genetics Baltimore, Maryland, USA October 28-November 1, 1997
ISSN: 0002-9297.
DT Conference
LA English
CC Genetics and Cytogenetics - Human *03508
General Biology - Information, Documentation, Retrieval and Computer Applications *00530
Radiation - General *06502
Biochemical Studies - General *10060
Enzymes - General and Comparative Studies; Coenzymes *10802
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
cytochrome P2C19 gene: polymorphism; cytochrome P2D6 gene: polymorphism; cytochrome P450: polymorphic variant; DNAse
IT Methods & Equipment
confocal fluorescence scanning: analytical method; cytochrome P450 genotyping assay: **GeneChip** probe, genetic method, high

density oligonucleotide probe; terminal deoxynucleotidyl transferase labelling: analytical method; **GeneChip** software: computer software; PCR [polymerase chain reaction]: DNA amplification method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 9035-51-2 (CYTOCHROME P450)
9003-98-9 (DNASE)
9027-67-2 (TERMINAL DEOXYNUCLEOTIDYL TRANSFERASE)

L38 ANSWER 22 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1994:526325 BIOSIS
DN PREV199497539325
TI Detection of cystic fibrosis mutations in a **GeneChip**-TM assay format.
AU Miyada, C. G.; Cronin, M. T.; Kim, S. M.; Fucini, R. V.; Masino, R. S.; Wespi, R. M.
CS **Affymetrix**, Santa Clara, CA 95051 USA
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A362.
Meeting Info.: 44th Annual Meeting of the American Society of Human Genetics Montreal, Quebec, Canada October 18-22, 1994
ISSN: 0002-9297.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biophysics - Molecular Properties and Macromolecules *10506
Pathology, General and Miscellaneous - Diagnostic *12504
Metabolism - Metabolic Disorders *13020
Respiratory System - Pathology *16006
Developmental Biology - Embryology - Pathological *25503
BC Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Development; Genetics; Metabolism; Pathology; Pulmonary Medicine (Human Medicine, Medical Sciences)
IT Miscellaneous Descriptors
CHIP SURFACE; DNA HYBRIDIZATION; MEETING ABSTRACT; MOLECULAR DIAGNOSTICS; MOLECULAR GENETICS; MUTANT SEQUENCE
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L38 ANSWER 23 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1994:525466 BIOSIS
DN PREV199497538466
TI **GeneChip** screening assay for cystic fibrosis mutations.
AU Cronin, M. T.; Miyada, C. G.; Fucini, R. V.; Kim, S. M.; Masino, R. S.; Wespi, R. M.
CS **Affymetrix**, Santa Clara, CA 95051 USA
SO American Journal of Human Genetics, (1994) Vol. 55, No. 3 SUPPL., pp. A217.
Meeting Info.: 44th Annual Meeting of the American Society of Human Genetics Montreal, Quebec, Canada October 18-22, 1994
ISSN: 0002-9297.

DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - Human *03508
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biophysics - General Biophysical Techniques *10504
Biophysics - Molecular Properties and Macromolecules *10506
BC Hominidae *86215
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Methods and Techniques
IT Miscellaneous Descriptors
ANALYTICAL METHOD; CYSTIC FIBROSIS TRANSMEMBRANE CONDUCTANCE REGULATOR; DNA; MEETING ABSTRACT; MEETING POSTER; MUTATION ANALYSIS
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L38 ANSWER 24 OF 24 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1994:327893 BIOSIS
DN PREV199497340893
TI Detection of cystic fibrosis gene mutations by hybridization to **GeneChip** probe arrays.
AU Cronin, M. T.; Barniv, Z.; Morris, M. S.; Hubbell, E.; Lobban, P.; Gentalen, E.; Miyada, C. G.; Chee, M.; Shah, N.; Masino, R.; Fodor, S. P. A.
CS **Affymetrix**, Santa Clara, CA 95051 USA
SO Clinical Chemistry, (1994) Vol. 40, No. 4, pp. 656.
Meeting Info.: 8th San Diego Conference on Beyond DNA Probes San Diego, California, USA November 18-20, 1993
ISSN: 0009-9147.
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biophysics - General Biophysical Techniques *10504
Pathology, General and Miscellaneous - Diagnostic *12504
BC Hominidae *86215
IT Major Concepts
Genetics; Methods and Techniques; Pathology
IT Miscellaneous Descriptors
DNA; MEETING ABSTRACT; MEETING POSTER; MOLECULAR DIAGNOSTIC METHOD
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

=> d all tot

L50 ANSWER 1 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:50678 BIOSIS
DN PREV200100050678
TI **Genechip** measurements and regulation of activated T cell death by members of the NF-kB/Rel family.

AU Mitchell, T. (1); Teague, T. K. (1); Hildeman, D. (1); Kedl, R. M. (1); White, J. (1); Schaefer, B. C. (1); Rees, W. (1); Bender, J. (1); Kappler, J. (1); Marrack, P. (1)
CS (1) Howard Hughes Medical Institute, National Jewish Medical and Research Center, Denver, CO USA
SO FASEB Journal, (April 20, 2000) Vol. 14, No. 6, pp. A1221. print.
Meeting Info.: Joint Annual Meeting of the American Association of Immunologists and the Clinical Immunology Society Seattle, Washington, USA May 12-16, 2000
ISSN: 0892-6638.
DT Conference
LA English
SL English
CC Immunology and Immunochemistry - General; Methods *34502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Cytology and Cytochemistry - General *02502
Cytology and Cytochemistry - Animal *02506
Blood, Blood-Forming Organs and Body Fluids - Blood and Lymph Studies *15002
Blood, Blood-Forming Organs and Body Fluids - Blood Cell Studies *15004
Virology - Animal Host Viruses *33506
IT Major Concepts
Cell Biology; Immune System (Chemical Coordination and Homeostasis); Methods and Techniques
IT Parts, Structures, & Systems of Organisms
T cell: blood and lymphatics, immune system
IT Chemicals & Biochemicals
NF-kappa B/Rel family members
IT Methods & Equipment
Genechip hybridization analysis: analytical method
IT Miscellaneous Descriptors
T cell homeostasis; activated T cell death: **Genechip** measurements, regulation; immune response-related cell survival; Meeting Abstract
ORGN Super Taxa
Poxviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
vaccinia virus (Poxviridae)
ORGN Organism Superterms
Animal Viruses; Microorganisms; Viruses

L50 ANSWER 2 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:37808 BIOSIS
DN PREV200100037808
TI Suicidal differential housekeeping gene activity in apoptosis induced by DCNP.
AU Qi, L.; Sit, K. H. (1)
CS (1) Anatomy Department, Faculty of Medicine, National University of Singapore, Kent Ridge, Singapore, 117597: antsitkh@nus.edu.sg Singapore
SO Apoptosis, (October, 2000) Vol. 5, No. 4, pp. 379-388. print.
ISSN: 1360-8185.
DT Article
LA English
SL English
AB Previous suggestions of CpG-specific apoptotic commitment implied critical epigenetic modulation of housekeeping genes which have canonical CpG islands at 5' promoter regions. Differential housekeeping gene activity however has not been shown. Using a focussed **microarray** (**genechip**) of 22 housekeeping genes we show this in apoptosis induced in human Chang liver cells by DCNP (2,6-dichloro-4-nitrophenol), a non-genotoxic inhibitor of sulfate detoxification. 3-7 folds downregulation of 9 genes in glycolysis, tricarboxylic acid cycle and the respiratory electron transport chain suggested gene-directed energy depletion which was correlated with observed ATP depletion. 4 folds downregulation of the pyruvate dehydrogenease gene suggested gene-directed

metabolic acidosis which was correlated with observed cell acidification. Other differential housekeeping gene activity, including 4 folds upregulation of microtubular alpha-tubulin gene, and 2 folds upregulation of ubiquitin, also had a bearing on apoptosis. Broadspectrum zVAD-fmk caspase inhibition abolished 200 bp DNA ladder fragmentations but not the CpG-specific megabase fragmentations and other hallmarks of cell destruction, suggesting a caspase-independent cell death. Death appeared committed at gene-level.

CC Genetics and Cytogenetics - General *03502
Cytology and Cytochemistry - General *02502
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508

IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology

IT Chemicals & Biochemicals
2,6-dichloro-4-nitrophenol; housekeeping gene: suicidal-differential activity; zVAD-fmk caspase

IT Methods & Equipment
genechip microarray: equipment

IT Miscellaneous Descriptors
apoptosis; cell acidification; cell death

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
Chang liver cell line (Hominidae)

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

RN 618-80-4 (2,6-DICHLORO-4-NITROPHENOL)

L50 ANSWER 3 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS

AN 2001:37686 BIOSIS

DN PREV200100037686

TI Over-expression of human UDP-glucose pyrophosphorylase rescues galactose-1-phosphate uridyl transferase deficient yeast.

AU Elsas, L. J. (1); Lai, K. (1)

CS (1) Division of Medical Genetics, Department of Pediatrics, Emory University, Atlanta, GA USA

SO Journal of Inherited Metabolic Disease, (July, 2000) Vol. 23, No. Supplement 1, pp. 158. print.
Meeting Info.: VIIIth International Conference on Inborn Errors of Metabolism England, Cambridge, UK September 13-17, 2000
ISSN: 0141-8955.

DT Conference

LA English

SL English

CC Genetics and Cytogenetics - Plant *03504
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Human *03508
Clinical Biochemistry; General Methods and Applications *10006
Metabolism - Metabolic Disorders *13020
Blood, Blood-Forming Organs and Body Fluids - Blood, Lymphatic and Reticuloendothelial Pathologies *15006

BC Fungi - Unspecified 15000

IT Major Concepts
Clinical Chemistry (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Diseases
galactosemia: blood and lymphatic disease, genetic disease, metabolic disease, treatment

IT Chemicals & Biochemicals
UDP-glucose phosphorylase: accumulation, expression, regulation; galactose regulon: regulation; galactose-1-phosphate uridyltransferase: accumulation, deficiency

IT Alternate Indexing
Galactosemia (MeSH)
IT Methods & Equipment
Ye6100 **GeneChip: computer software;**
galactose medium: laboratory equipment
IT Miscellaneous Descriptors
metabolic blockade; Meeting Abstract
ORGN Super Taxa
Fungi: Plantae
ORGN Organism Name
yeast (Fungi): GALT-knocked out, strain-revertant, wild-type
ORGN Organism Superterms
Fungi; Microorganisms; Nonvascular Plants; Plants
RN 9026-22-6 (UDP-GLUCOSE PHOSPHORYLASE)
9016-11-9 (GALACTOSE-1-PHOSPHATE URIDYLTRANSFERASE)

L50 ANSWER 4 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2001:5537 BIOSIS
DN PREV200100005537
TI DNA **microarray** analysis of mRNA expression in psoriatic skin.
AU Johnson, C. M. (1); Mee, J. B.; Burslem, F. (1); Groves, R. W.
CS (1) Discovery Biology, Pfizer Central Research, Sandwich, Kent UK
SO Journal of Investigative Dermatology, (September, 2000) Vol. 115, No. 3, pp. 576. print.
Meeting Info.: Abstracts for the 30th European Society for Dermatological Research Annual Meeting Berlin, Germany September 21-23, 2000
ISSN: 0022-202X.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - General *03502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Integumentary System - Pathology *18506
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Dermatology (Human Medicine, Medical Sciences)
IT Diseases
chronic plaque psoriasis: integumentary system disease
IT Chemicals & Biochemicals
mRNA [messenger RNA]: psoriatic lesional skin expression
IT Methods & Equipment
DNA **microarray** analysis [**GeneChip** analysis]:
genetic method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 5 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:540656 BIOSIS
DN PREV200000540656
TI p53 **genechip** assay, **computerized mutation** analysis and gene sequencing.
AU Halachmi, Sarel (1); Ahrendt, Steve (1); Chow, John T. (1); Halachmi, Naomil (1); Yang, Stephan C. (1); Wehage, Scott (1); Nativ, Ofer; Sidransky, David (1)
CS (1) Head and Neck Research Division, Johns Hopkins Hospital, Baltimore, MD USA
SO European Urology, (October, 2000) Vol. 38, No. 4, pp. 508. print.

Meeting Info.: 15th Congress of the European Society for Urological Research Istanbul, Turkey October 05-07, 2000
ISSN: 0302-2838.
DT Conference
LA English
SL English
CC Urinary System and External Secretions - Physiology and Biochemistry *15504
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Urinary System and External Secretions - Pathology *15506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Urinary System (Chemical Coordination and Homeostasis); Methods and Techniques
IT Diseases
bladder cancer: neoplastic disease, urologic disease; cancer: neoplastic disease
IT Chemicals & Biochemicals
p53: **mutation**
IT Alternate Indexing
Bladder Neoplasms (MeSH)
IT Methods & Equipment
computerized mutation analysis: analytical method; gene sequencing: analytical method, cycle DNA sequencing; p53 **genechip** assay: analytical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 6 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:514637 BIOSIS
DN PREV200000514637
TI Comparison of p53 immunohistochemical staining patterns with dideoxynucleotide sequencing and p53 **GeneChip** assay in primary lung cancer.
AU Dintzis, S. M. (1); Swanson, P. E. (1); Ahrendt, S. A.; Wu, L.; Yang, S. C.; Sidransky, D.
CS (1) Washington University School of Medicine, St. Louis, MO USA
SO Laboratory Investigation, (March, 2000) Vol. 80, No. 3, pp. 221A. print.
Meeting Info.: Annual Meeting of the United States and Canadian Academy of Pathology New Orleans, Louisiana, USA March 25-31, 2000
ISSN: 0023-6837.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
Respiratory System - Physiology and Biochemistry *16004
Respiratory System - Pathology *16006
Neoplasms and Neoplastic Agents - Diagnostic Methods *24001
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Neoplasms and Neoplastic Agents - Therapeutic Agents; Therapy *24008
IT Major Concepts

Molecular Genetics (Biochemistry and Molecular Biophysics); Respiratory System (Respiration); Tumor Biology
IT Diseases
primary lung cancer: diagnosis, neoplastic disease, respiratory system disease, treatment
IT Chemicals & Biochemicals
p53; p53 immunohistochemistry staining: analytical method; human p53 gene (Hominidae)
IT Alternate Indexing
Lung Neoplasms (MeSH)
IT Methods & Equipment
dideoxynucleotide sequencing: genetic method; p53 **GeneChip** assay: analytical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 7 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:513590 BIOSIS
DN PREV200000513590
TI Identifying candidate genes for mania and psychosis using a convergent functional **genomics** approach.
AU Niculescu, A. B., III (1); Segal, D. S. (1); Kuczenski, R. (1); Barrett, T. (1); Hauger, R. (1); Kelsoe, J. R. (1)
CS (1) Department of Psychiatry, UCSD School of Medicine, 9500 Gilman Drive, 0603-R, La Jolla, CA, 92093-0603 USA
SO American Journal of Medical Genetics, (August 7, 2000) Vol. 96, No. 4, pp. 481. print.
Meeting Info.: Eigth World Congress on Psychiatric Genetics Versailles, France August 27-31, 2000 International Society of Psychiatric Genetics . ISSN: 0148-7299.
DT Conference
LA English
SL English
CC Biochemical Studies - General *10060
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - Human *03508
Behavioral Biology - Human Behavior *07004
Pathology, General and Miscellaneous - Therapy *12512
Psychiatry - Psychopathology; Psychodynamics and Therapy *21002
Pharmacology - Clinical Pharmacology *22005
Pharmacology - Psychopharmacology *22026
IT Major Concepts
Medical Genetics (Allied Medical Sciences); Psychiatry (Human Medicine, Medical Sciences)
IT Diseases
bipolar disorder: behavioral and mental disorders; mania: behavioral and mental disorders; psychosis: behavioral and mental disorders; schizophrenia: behavioral and mental disorders
IT Chemicals & Biochemicals
amphetamine: antipsychotic - drug
IT Alternate Indexing
Bipolar Disorder (MeSH); Psychotic Disorders (MeSH); Schizophrenia (MeSH)
IT Methods & Equipment
oligonucleotide **GeneChip microarray**: expression method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa

Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 300-62-9 (AMPHETAMINE)

L50 ANSWER 8 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:512669 BIOSIS
DN PREV200000512669
TI High-**density microarray genechip** analysis reveals different gene expression profiles in hepatitis B and C induced hepatocellular carcinoma.
AU Kaiser, Stephan (1); Gregor, Michael (1); Hwang, Jungjoo
CS (1) Univ of Tuebingen, Tuebingen Germany
SO Hepatology, (October, 2000) Vol. 32, No. 4 Pt. 2, pp. 320A. print.
Meeting Info.: 51st Annual Meeting and Postgraduate Courses of the American Association for the Study of Liver Diseases Dallas, Texas, USA October 27-31, 2000 American Association for the Study of Liver Diseases . ISSN: 0270-9139.
DT Conference
LA English
SL English
CC Digestive System - Physiology and Biochemistry *14004
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Digestive System - Pathology *14006
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
Genetics of Bacteria and Viruses *31500
Virology - Animal Host Viruses *33506
Medical and Clinical Microbiology - Virology *36006
BC Flaviviridae 02609
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Infection; Digestive System (Ingestion and Assimilation); Tumor Biology
IT Diseases
hepatocellular carcinoma: digestive system disease, neoplastic disease
IT Alternate Indexing
Carcinoma, Hepatocellular (MeSH)
IT Methods & Equipment
high-**density microarray genechip**
analysis: detection method, gene expression analytical method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Flaviviridae: Animal Viruses, Viruses, Microorganisms; Hepadnaviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
hepatitis B (Hepadnaviridae): pathogen; hepatitis C (Flaviviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Microorganisms; Viruses

L50 ANSWER 9 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:491210 BIOSIS
DN PREV200000491331
TI Validation of expression profiling: Effect of multiple tests, and use of antibody confirmation on patient tissues with known genetic defect.
AU Zhao, P. (1); Chen, Y.-W. (1); Vivanco, F.; Lawler, J.; Hoffman, E. P. (1)
CS (1) Research Center for Genetic Medicine, CNMC, Washington, DC USA
SO American Journal of Human Genetics, (October, 2000) Vol. 67, No. 4 Supplement 2, pp. 397. print.
Meeting Info.: 50th Annual Meeting of the American Society of Human Genetics Philadelphia, Pennsylvania, USA October 03-07, 2000 American

Society of Human Genetics
. ISSN: 0002-9297.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Enzymes - General and Comparative Studies; Coenzymes *10802
Muscle - Physiology and Biochemistry *17504
Muscle - Pathology *17506
Nervous System - Pathology *20506
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Parts, Structures, & Systems of Organisms
muscle: muscular system
IT Diseases
DMD [Duchenne muscular dystrophy]: muscle disease, nervous system disease; genetic defect: genetic disease
IT Chemicals & Biochemicals
RNA; phospholipase A2
IT Methods & Equipment
GeneChip data: analytical method
IT Miscellaneous Descriptors
antibody confirmation; expression profiling; Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 10 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:478465 BIOSIS
DN PREV200000478465
TI Housekeeping genes commanded to commit suicide in CpG-cleavage commitment upstream of Bcl-2 inhibition in caspase-dependent and -independent pathways.
AU Qi, L.; Sit, K. H. (1)
CS (1) Department of Anatomy, Faculty of Medicine, National University of Singapore, 4 Medical Drive, Kent Ridge, Singapore, 117597 Singapore
SO Molecular Cell Biology Research Communications, (May, 2000) Vol. 3, No. 5, pp. 319-327. print.
ISSN: 1522-4724.
DT Article
LA English
SL English
AB A CpG-specific commitment common to both caspase-dependent and -independent cell deaths implies critical gene activity from epigenetic modulation. Using a focused **microarray** (**genechip**) of 22 housekeeping genes, which have canonical CpG islands at 5'-promoter regions, here we show critical regulation of vital intermediary metabolism and cell structure that are common to both caspase-dependent fasL-mediated and caspase-independent etoposide-mediated cell deaths. Gene activity of at least twofold under or over control levels and common to both cell death pathways was considered to be significantly regulated in common. Seven genes controlling energy production in glycolysis, tricarboxylic acid cycle, and the respiratory electron transport chain were significantly downregulated in common. Energy depletion is lethal. Downregulated pyruvate dehydrogenase E1 gene, in addition, suggested primary metabolic acidification. Cell acidification is also lethal. Critical derangement of the cell structure was suggested by common

downregulation of the basal histone gene H2A.X which is required for nucleosome assembly. Common upregulation of the alpha-tubulin gene suggested perturbation of vital microtubular dynamics. Gene-commanded cell suicide was suggested. We further show that a Bcl-2 overexpression of three- to fourfold above normal levels could not prevent the CpG-specific megabase DNA cleavages in the two cell death pathways, but abolished their low-molecular-weight 200-bp ladder cleavages. Together with incomplete suppression of the other apoptotic expressions, the Bcl-2 inhibition point appeared downstream from the CpG-cleavage commitment point.

CC Genetics and Cytogenetics - Human *03508
Cytology and Cytochemistry - General *02502
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - Proteins, Peptides and Amino Acids *10064

IT Major Concepts
Biochemistry and Molecular Biophysics; Molecular Genetics (Biochemistry and Molecular Biophysics); Cell Biology

IT Chemicals & Biochemicals
Bcl-2: inhibition; DNA: cleavage; FasL [Fas ligand]; etopside: caspase-independent activity, cell death; tricarboxylic acid; H2A.X gene: basal histone gene; alpha-tubulin gene: upregulation; pyruvate dehydrogenase E1 gene: downregulation

IT Miscellaneous Descriptors
CpG-specific commitment; cell death pathway; cell wall; energy depletion; focused **microarray** [**genechip**]; glycolysis; housekeeping genes; respiratory electron transport chain; vital intermediate metabolism

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
LN18 cell line (Hominidae): human glioma cells

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 11 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:477729 BIOSIS
DN PREV200000477729
TI Laser capture microdissection-generated target sample for high-**density** oligonucleotide **array hybridization**.
AU Ohyama, H.; Zhang, X.; Kohno, Y.; Alevizos, I.; Posner, M.; Wong, D. T.; Todd, R. (1)
CS (1) Department of Oral and Maxillofacial Surgery, Warren 1201, Massachusetts General Hospital, 1 Fruit Street, Boston, MA, 02114 USA
SO Biotechniques, (September, 2000) Vol. 29, No. 3, pp. 530-536. print. ISSN: 0736-6205.
DT Article
LA English
SL English
AB Current advances in biomolecular technology allow precise genetic fingerprinting of specific cells responsible for the pathogenesis of human diseases. This study demonstrates the feasibility of generating target samples from laser capture microdissection (LCM) tissues suitable for **hybridization** of high-**density** oligonucleotide **arrays** for gene expression profiling. RNA was successfully isolated by LCM from three paired specimens of oral cancer and linearly amplified using T7 RNA polymerase. Evaluation of the cDNA revealed that five of five cellular maintenance transcripts are detected. Biotinylated cRNA was generated and **hybridized** to the human Test 1 **GeneChip**(R) **probe arrays**, which demonstrated that the RNA is of sufficient quality and integrity to warrant further analysis. Subsequent **hybridization** of the samples to the HuGenFL **GeneChip probe arrays** revealed that 26.5%-33.0% of the approximately 7000 represented genes are expressed in each of the six samples. These results demonstrate that LCM-generated

tissues can generate sufficient quality cRNA for high-**density** oligonucleotide **microarray** analysis, an important step in determining comprehensive gene expression profiling using this high-throughput technology.

CC Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Biochemical Studies - General *10060
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004

IT Major Concepts
Biochemistry and Molecular Biophysics; Methods and Techniques

IT Diseases
oral cancer: neoplastic disease

IT Chemicals & Biochemicals
RNA; T7 RNA polymerase; cDNA [complementary DNA]

IT Alternate Indexing
Mouth Neoplasms (MeSH)

IT Methods & Equipment
RNeasy Kit: Qiagen, laboratory equipment; Test 1 **GeneChip probe array**: laboratory equipment; high-**density** oligonucleotide **array hybridization**
: Molecular Biology Techniques and Chemical Characterization, analytical method; laser capture microdissection: Preparatory and General Laboratory Techniques, preparation method

IT Miscellaneous Descriptors
target samples

L50 ANSWER 12 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:437744 BIOSIS
DN PREV200000437744
TI Detection of aberrations of 17p and p53 gene in gastrointestinal cancers by dual (two-color) fluorescence in situ **hybridization** and **GeneChip** p53 assay.
AU Takahashi, Yasuo (1); Nagata, Toshihito; Asai, Satoshi; Shintaku, Kaori; Eguchi, Teruo; Ishii, Yukimoto; Fujii, Masashi; Ishikawa, Koichi
CS (1) Department of Pharmacology, Nihon University School of Medicine, 30 Oyaguchi-Kami Machi, Itabashi, Tokyo, 173-8610 Japan
SO Cancer Genetics and Cytogenetics, (August, 2000) Vol. 121, No. 1, pp. 38-43. print.
ISSN: 0165-4608.
DT Article
LA English
SL English
AB We performed dual (two-color) fluorescence in situ **hybridization** (FISH) using direct fluorescent labeling **probes** for p53 and chromosome 17 in six gastrointestinal (3 stomach and 3 colon) cancers. In three of these (1 stomach and 2 colon) the interphase cell nuclei showed an imbalance of signals for the p53 and chromosome 17; that is, the p53 signal count was lower than the chromosome 17 signal count, indicating **deletion** of the p53 gene. Moreover, metaphase FISH analysis demonstrated that those nuclei actually had a chromosome 17 with **deletion** of the p53 gene. Interestingly, these three cases had an abnormal chromosome 17 copy number, that is, chromosome 17 aneusomy. Furthermore, to investigate the possibility of p53 **mutation** in tumors with an imbalance of signals for chromosome 17 and p53 per nucleus, we performed a **GeneChip** p53 assay which has recently been developed. **GeneChip** p53 assay demonstrated that a primary tumor sample from one colon cancer case had a heterozygous point **mutation** of CGT (Arg) to CAT (His) at codon 273 in exon 8. In addition, a sample of metastatic tumor in the liver from the same case revealed two heterozygous point **mutations**. One of them was the same **mutation** as that is the primary tumor; the other was GTG (Val) to GGG (Gly) at codon 217 in exon 6. In conclusion, we found that the combination of dual-color FISH and **GeneChip** p53 assay offered reliable results and important information concerning not only **deletion** of the p53 gene and chromosome 17 aneusomy but also p53 **mutations**. Using these techniques, we demonstrated that an

imbalance of signals for chromosome 17 and p53 per nucleus, chromosome 17 aneusomy, and accumulation of p53 **mutations** had occurred during carcinogenesis and development of gastrointestinal cancers.
CC Digestive System - Physiology and Biochemistry *14004
Genetics and Cytogenetics - Human *03508
Digestive System - Pathology *14006
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Medical Genetics (Allied Medical Sciences); Digestive System (Ingestion and Assimilation); Methods and Techniques; Tumor Biology
IT Parts, Structures, & Systems of Organisms
chromosome 17: copy number; colon: digestive system; stomach: digestive system
IT Diseases
gastrointestinal cancers: digestive system disease, neoplastic disease
IT Chemicals & Biochemicals
human p53 gene (Hominidae): aberrations
IT Methods & Equipment
direct fluorescent labeling **probes**: analytical method; dual fluorescence in situ **hybridization** [dual FISH]: genetic method; **genechip** p53 assay: genetic method
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 13 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:428893 BIOSIS
DN PREV200000428893
TI Intracrine signaling by PTHrP regulates a complex pattern of growth-affecting genes in prostate cancer.
AU Wachsman, W. (1); Gujral, A. (1); Burton, D. (1); Deftos, L. J. (1)
CS (1) Department of Medicine and Cancer Centers, UCSD and SDVAMC, San Diego, CA USA
SO Journal of Bone and Mineral Research, (September, 2000) Vol. 15, No. Suppl. 1, pp. S568. print.
Meeting Info.: Twenty-Second Annual Meeting of the American Society for Bone and Mineral Research Toronto, Ontario, Canada September 22-26, 2000 American Society for Bone and Mineral Research
. ISSN: 0884-0431.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
Urinary System and External Secretions - Pathology *15506
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004
IT Major Concepts
Biochemistry and Molecular Biophysics; Genetics; Tumor Biology
IT Diseases
prostate cancer: neoplastic disease, reproductive system disease/male, urologic disease
IT Chemicals & Biochemicals
growth-affecting genes: complex pattern; parathyroid hormone related protein
IT Alternate Indexing
Prostatic Neoplasms (MeSH)

IT Methods & Equipment
GeneChip high-**density** oligonucleotide-based **arrays**: analytical method
IT Miscellaneous Descriptors
intracrine signaling; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
PPC-1 cell line (Hominidae): human prostate cancer cell line
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 14 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:418810 BIOSIS
DN PREV200000418810
TI Development of an affymetrixTM 16S rRNA **GeneChip** for bacterial identification.
AU Wilson, W. J. (1); Viswanathan, V. (1); Macht, M. (1); Wilson, K. H.; Andersen, G. L. (1)
CS (1) Lawrence Livermore National Laboratory, Livermore, CA USA
SO Abstracts of the General Meeting of the American Society for Microbiology, (2000) Vol. 100, pp. 546-547. print.
Meeting Info.: 100th General Meeting of the American Society for Microbiology Los Angeles, California, USA May 21-25, 2000 American Society for Microbiology
. ISSN: 1060-2011.
DT Conference
LA English
SL English
CC Physiology and Biochemistry of Bacteria *31000
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
Genetics and Cytogenetics - General *03502
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines *10062
Genetics of Bacteria and Viruses *31500
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques
IT Chemicals & Biochemicals
16S ribosomal RNA gene; AffymetrixTM 16S rRNA **GeneChip** [AffymetrixTM 16S ribosomal RNA **GeneChip**]; DNA; SAPE: fluorescent dye
IT Methods & Equipment
bacterial identification: analytical method; laser confocal microscopy: microscopy method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Bacteria: Microorganisms
ORGN Organism Name
bacteria (Bacteria)
ORGN Organism Superterms
Bacteria; Eubacteria; Microorganisms

L50 ANSWER 15 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:346540 BIOSIS
DN PREV200000346540
TI Determination of genes involved in the process of implantation: Application of **GeneChip** to scan 6500 genes.
AU Yoshioka, Ken-ichi; Matsuda, Fuko; Takakura, Kenji; Noda, Youichi; Imakawa, Kazuhiko (1); Sakai, Senkiti
CS (1) Laboratory of Animal Breeding, University of Tokyo, 1-1-1 Yayoi, Bunkyo-ku, Tokyo, 113-8657 Japan
SO Biochemical and Biophysical Research Communications, (June 7, 2000) Vol. 272, No. 2, pp. 531-538. print.
ISSN: 0006-291X.

DT Article
LA English
SL English
AB Using the high-**density arrays** of oligonucleotides (**GeneChip**) technology, the expression of uterine genes was examined before and after conceptus implantation in mice. Of the 6500 genes analyzed, levels of 399 gene expressions changed; 192 genes increased levels of expression while the remaining 207 genes declined. The findings suggest that both gene activation and deactivation (suppression) are required for successful implantation.
CC Developmental Biology - Embryology - General and Descriptive *25502
Genetics and Cytogenetics - General *03502
Genetics and Cytogenetics - Animal *03506
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Development; Methods and Techniques
IT Methods & Equipment
GeneChip: determination method
IT Miscellaneous Descriptors
gene expression; implantation
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
mouse (Muridae): conceptus, female
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates

L50 ANSWER 16 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:314394 BIOSIS
DN PREV200000314394
TI **Microarray genechip** analysis of altered gene expression profiles in Hepatitis C - induced hepatocellular carcinoma.
AU Kaiser, S.; Hwang, J. J.; Gregor, M.
SO Journal of Hepatology, (2000) Vol. 32, No. Supplement 2, pp. 164. print. Meeting Info.: 35th Annual Meeting of the European Association for the Study of the Liver Rotterdam, Netherlands April 29-May 03, 2000 European Association for the Study of the Liver
. ISSN: 0168-8278.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Digestive System - General; Methods *14001
Medical and Clinical Microbiology - General; Methods and Techniques *36001
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Flaviviridae 02609
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Digestive System (Ingestion and Assimilation); Tumor Biology
IT Diseases
hepatitis C: digestive system disease, viral disease; hepatocellular carcinoma: digestive system disease, neoplastic disease
IT Chemicals & Biochemicals
genes: expression
IT Alternate Indexing
Hepatitis C (MeSH); Carcinoma, Hepatocellular (MeSH)
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification, analytical method, in-situ recombinant gene expression detection, sequencing techniques; **microarray genechip** analysis: analytical method
IT Miscellaneous Descriptors

disease screening; tumorigenesis; Meeting Abstract
ORGN Super Taxa
Flaviviridae: Animal Viruses, Viruses, Microorganisms; Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
hepatitis C virus (Flaviviridae): pathogen; human (Hominidae): patient
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L50 ANSWER 17 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:291386 BIOSIS
DN PREV200000291386
TI Relationship of paroxetine disposition to metoprolol metabolic ratio and CYP2D6*10 genotype of Korean subjects.
AU Yoon, Young-Ran; Cha, In-June; Shon, Ji-Hong; Kim, Kyung-Ah; Cha, Young-Nam; Jang, In-Jin; Park, Chan-Woong; Shin, Sang-Goo; Flockhart, David A.; Shin, Jae-Gook
SO Clinical Pharmacology & Therapeutics, (May, 2000) Vol. 67, No. 5, pp. 567-576. print..
ISSN: 0009-9236.
DT Article
LA English
SL English
AB Objective: To evaluate the relationship between the metabolic ratio (MR) of metoprolol, CYP2D6*10B genotype, and the disposition of paroxetine in Korean subjects. Methods: A single 40-mg dose of paroxetine was administered orally to one poor metabolizer and 15 healthy subjects recruited from 223 Korean extensive metabolizers whose phenotypes were predetermined by use of the metoprolol MR. Genotypes were determined by allele-specific polymerase chain reaction and the **GeneChip microarray** technique. Pharmacokinetic parameters were estimated from plasma concentrations of paroxetine for more than 240 hours after the oral dose. Results: The oral clearance and area under the plasma concentration versus time curve (AUC) of paroxetine were best described by a nonlinear relationship with metoprolol MR at correlation coefficients of 0.82 and 0.91, respectively ($P < .05$). Nine extensive metabolizer who were either homozygous or heterozygous for CYP2D6*10B had significantly lower oral clearance values of paroxetine than six extensive metabolizers with CYP2D6*1/*1. The AUC of paroxetine in subjects who were homozygous for CYP2D6*10B (666.4 +- 169.4 ng/mL cntdot h) was significantly greater than that of subjects who were homozygous for the wild type (194.5 +- 55.9 ng/mL cntdot h). Unexpectedly, the average AUC of subjects who were heterozygous for CYP2D6*10B was greater with wide variation (789.8 +- 816.9 ng/mL cntdot h) than that of subjects who were homozygous CYP2D6*10B/*10B mainly because of two atypical subjects whose metoprolol MR was not associated with the CYP2D6*10B genotype and who showed greater AUC and lower oral clearance than subjects with homozygous CYP2D6*10B. Conclusions: The CYP2D6 activity measured by metoprolol MR was a strong predictor of paroxetine disposition in Korean extensive metabolizers. In general, the extensive metabolizers with the CYP2D6*10B allele seemed to have higher plasma concentrations of paroxetine than extensive metabolizers with the wild-type CYP2D6 genotype. However, quantitative prediction of paroxetine disposition from the CYP2D6*10B genotype alone was not perfect because several Korean extensive metabolizers had metoprolol MRs that were not associated with the genotype.
CC Pharmacology - General *22002
Genetics and Cytogenetics - Human *03508
Genetics and Cytogenetics - Population Genetics *03509
Enzymes - Chemical and Physical *10806
Metabolism - General Metabolism; Metabolic Pathways *13002
Biochemical Studies - General *10060
Biochemical Studies - Proteins, Peptides and Amino Acids *10064
IT Major Concepts
Enzymology (Biochemistry and Molecular Biophysics); Pharmacology; Population Genetics (Population Studies)

IT Chemicals & Biochemicals
CYP2D6 10 [cytochrome P450 2D6 10]; metoprolol; paroxetine
IT Miscellaneous Descriptors
genotype
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): Korean
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates
RN 51384-51-1 (METOPROLOL)
61869-08-7 (PAROXETINE)

L50 ANSWER 18 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:276011 BIOSIS
DN PREV200000276011
TI High-**density microarray genechip** analysis reveals different gene expression profiles in hepatoma cell lines and in hepatocellular carcinoma tissue.
AU Kaiser, Stephan (1); Hwang, Jungjoo; Gregor, Michael
CS (1) Univ of Tuebingen, Tuebingen Germany
SO Gastroenterology, (April, 2000) Vol. 118, No. 4 Suppl. 2 Part 1, pp. AASLD A905. print..
Meeting Info.: 101st Annual Meeting of the American Gastroenterological Association and the Digestive Disease Week. San Diego, California, USA May 21-24, 2000 American Gastroenterological Association
. ISSN: 0016-5085.
DT Conference
LA English
SL English
CC Neoplasms and Neoplastic Agents - General *24002
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
Digestive System - General; Methods *14001
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Digestive System (Ingestion and Assimilation); Tumor Biology
IT Diseases
hepatocellular carcinoma: digestive system disease, neoplastic disease; hepatoma: digestive system disease, neoplastic disease
IT Chemicals & Biochemicals
mRNA [messenger RNA]
IT Alternate Indexing
Carcinoma, Hepatocellular (MeSH)
IT Methods & Equipment
PCR [polymerase chain reaction]: DNA amplification method; high-**density microarray genechip** analysis:
analytical method
IT Miscellaneous Descriptors
gene expression; liver tumorigenesis; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
Hep3B cell line (Hominidae): human hepatoma cells; HepG2 cell line (Hominidae): human hepatoma cells; Huh-1 cell line (Hominidae): human hepatoma cells; Huh-7 cell line (Hominidae): human hepatoma cells; SK-Hep cell line (Hominidae): human hepatoma cells; human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 19 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:274392 BIOSIS
DN PREV200000274392

TI The transcriptional profile in cultured conjunctival epithelial cells induced by serum depletion.
AU Higuchi, A. (1); Shimmura, S. (1); Ishii, M.; Aburatani, H.; Kodama, T.; Tsubota, K. (1)
CS (1) Ophthalmology, Tokyo Dental College/Ichikawa Ge, Ichikawa, Chiba Japan
SO IOVS, (March 15, 2000) Vol. 41, No. 4, pp. S873. print..
Meeting Info.: Annual Meeting of the Association in Vision and Opthalmology. Fort Lauderlade, Florida, USA April 30-May 05, 2000 Association for Research in Vision and Ophthalmology
.
DT Conference
LA English
SL English
CC Sense Organs, Associated Structures and Functions - Physiology and Biochemistry *20004
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Biochemistry and Molecular Biophysics; Cell Biology; Sense Organs (Sensory Reception)
IT Parts, Structures, & Systems of Organisms
conjunctival epithelial cells: apoptosis, cultured, sensory system, transcriptional profile
IT Chemicals & Biochemicals
c-myc messenger RNA: expression; death domain receptor 3 messenger RNA: expression
IT Methods & Equipment
GeneChip: molecular genetic method
IT Miscellaneous Descriptors
serum depletion; Meeting Abstract; Meeting Poster

L50 ANSWER 20 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:266522 BIOSIS
DN PREV200000266522
TI Comparison of TP53 **mutations** identified by oligonucleotide **microarray** and conventional DNA sequence analysis.
AU Wen, Wen-Hsiang; Bernstein, Leslie; Lescallett, Jennifer; Beazer-Barclay, Yasmin; Sullivan-Halley, Jane; White, Marga; Press, Michael F. (1)
CS (1) USC/Norris Comprehensive Cancer Center, University of Southern California School of Medicine, 1441 Eastlake Avenue, Norris Topping Tower, Room 5409, Los Angeles, CA, 90033 USA
SO Cancer Research, (May 15, 2000) Vol. 60, No. 10, pp. 2716-2722. print..
ISSN: 0008-5472.
DT Article
LA English
SL English
AB As the rate of gene discovery accelerates, more efficient methods are needed to analyze genes in human tissues. To assess the efficiency, sensitivity, and specificity of different methods, alterations of TP53 were independently evaluated in 108 ovarian tumors by conventional DNA sequence analysis and oligonucleotide **microarray** (p53 **GeneChip**). All **mutations** identified by oligonucleotide **microarray** and all disagreements with conventional gel-based DNA sequence analysis were confirmed by re-analysis with manual and automated dideoxy DNA sequencing. A total of 77 ovarian cancers were identified as having TP53 **mutations** by one of the two approaches, 71 by **microarray** and 63 by gel-based DNA sequence analysis. The same **mutation** was identified in 57 ovarian cancers, and the same wild type TP53 sequence was observed in 31 ovarian cancers by both methods, for a concordance rate of 81%. Among the **mutation** analyses discordant by these methods for TP53 sequence were 14 cases identified as **mutated** by **microarray** but not by conventional DNA sequence analysis and 6 cases identified as **mutated** by conventional DNA sequence analysis but not by **microarray**. Overall, the oligonucleotide **microarray** demonstrated a 94% accuracy rate, a 92% sensitivity, and an 100% specificity. Conventional

DNA sequence analysis demonstrated an 87% accuracy rate, 82% sensitivity, and a 100% specificity. Patients with TP53 **mutations** had significantly shorter overall survival than those with no **mutation** (P = 0.02). Women with **mutations** in loop2, loop3, or the loop-sheet-helix domain had shorter survival than women with other **mutations** or women with no **mutations** (P = 0.01). Although further refinement would be helpful to improve the detection of certain types of TP53 alterations, oligonucleotide **microarrays** were shown to be a powerful and effective tool for TP53 **mutation** detection.

CC Genetics and Cytogenetics - Human *03508
Reproductive System - Physiology and Biochemistry *16504
Reproductive System - Pathology *16506
Neoplasms and Neoplastic Agents - Pathology; Clinical Aspects; Systemic Effects *24004

IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Reproductive System (Reproduction); Tumor Biology

IT Diseases
ovarian cancer: neoplastic disease, reproductive system disease/female

IT Chemicals & Biochemicals
human TP53 gene (Hominidae): **mutation**

IT Alternate Indexing
Ovarian Neoplasms (MeSH)

IT Methods & Equipment
conventional DNA sequence analysis: comparison, efficiency, genetic method, sensitivity, specificity; oligonucleotide **microarray**: comparison, efficiency, genetic method, sensitivity, specificity

IT Miscellaneous Descriptors
survival

ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia

ORGN Organism Name
human (Hominidae): female

ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 21 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:184613 BIOSIS
DN PREV200000184613
TI **Microarray** technology - enhanced versatility, persistent challenge.
AU Epstein, Charles B. (1); Butow, Ronald A. (1)
CS (1) Department of Molecular Biology, University of Texas Southwestern Medical Center, 5323 Harry Hines Boulevard, Dallas, TX, 75390-9148 USA
SO Current Opinion in Biotechnology, (Feb., 2000) Vol. 11, No. 1, pp. 36-41. ISSN: 0958-1669.
DT General Review
LA English
SL English
CC Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Genetics and Cytogenetics - General *03502

IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Methods and Techniques

IT Methods & Equipment
GeneChips: laboratory equipment; **microarray** analysis: analytical method

IT Miscellaneous Descriptors
gene dosage; **transcription** profiling

L50 ANSWER 22 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:156640 BIOSIS
DN PREV200000156640
TI Comparison of p53 immunohistochemical staining patterns with dideoxynucleotide sequencing and p53 **GeneChip** assay in primary

lung cancer.
AU Dintzis, S. M. (1); Swanson, P. E. (1); Ahrendt, S. A.; Wu, L.; Yang, S. C.; Sidransky, D.
CS (1) Washington University School of Medicine, Saint Louis, MO USA
SO Laboratory Investigation., (Jan., 2000) Vol. 80, No. 1, pp. 221A. Meeting Info.: 2000 Annual Meeting United States and Canadian Academy of Pathology. New Orleans, Louisiana, USA March 25-31, 2000 ISSN: 0023-6837.
DT Conference
LA English
SL English
CC Genetics and Cytogenetics - Human *03508
Microscopy Techniques - General and Special Techniques *01052
Anatomy and Histology, General and Comparative - Gross Anatomy *11102
Respiratory System - General; Methods *16001
Neoplasms and Neoplastic Agents - General *24002
Pathology, General and Miscellaneous - Diagnostic *12504
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Genetics; Oncology (Human Medicine, Medical Sciences); Methods and Techniques
IT Diseases
primary lung cancer: neoplastic disease, respiratory system disease
IT Chemicals & Biochemicals
p53 gene (Hominidae): immunohistochemical staining patterns
IT Alternate Indexing
Lung Neoplasms (MeSH)
IT Methods & Equipment
dideoxynucleotide sequencing: analytical method; immunohistochemistry: microscopy method; p53 **GeneChip** assay: analytical method, genetic method
IT Miscellaneous Descriptors
Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 23 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 2000:38413 BIOSIS
DN PREV200000038413
TI Prx1 and Prx2 homeodomain proteins: Identification and characterization of downstream targets.
AU Kubitz, Karen G. (1); Potter, S. Steven; Kern, Michael J. (1)
CS (1) Medical University of South Carolina, 500 MUSC Complex Suite 601, Charleston, SC, 29425 USA
SO Molecular Biology of the Cell, (Nov., 1999) Vol. 10, No. SUPPL., pp. 104a. Meeting Info.: 39th Annual Meeting of the American Society for Cell Biology Washington, D.C., USA December 11-15, 1999 The American Society for Cell Biology
. ISSN: 1059-1524.
DT Conference
LA English
CC Genetics and Cytogenetics - Animal *03506
Cytology and Cytochemistry - Animal *02506
Biophysics - General Biophysical Studies *10502
Enzymes - General and Comparative Studies; Coenzymes *10802
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
DNA; DNA binding proteins; PN-1 [protease nexin-1]; Prx1

[paired-related homeobox 1]; Prx2 [paired-related homeobox 2]; Prx1 gene [paired-related homeobox gene 1]; Prx2 gene [paired-related homeobox gene 2]; homeobox genes
IT Methods & Equipment
RT-PCR [reverse transcriptase-polymerase chain reaction]: analytical method, polymerase chain reaction; **genechip** technology: genetic method; northern blotting: analytical method; western blotting: analytical method
IT Miscellaneous Descriptors
downstream targets: identification; gene expression; Meeting Abstract
ORGN Super Taxa
Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
NIH3T3 cell line (Muridae)
ORGN Organism Superterms
Animals; Chordates; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Rodents; Vertebrates
RN 148196-69-4 (PROTEASE NEXIN-1)

L50 ANSWER 24 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:509167 BIOSIS
DN PREV199900509167
TI Large-scale detection and genotyping of mouse single-nucleotide polymorphisms.
AU Lindblad, K. (1); Patil, N.; Winchester, E. (1); Wang, D. (1); Robinson, E. (1); Daly, M. J. (1); Hirschhorn, J. (1); Sklar, P. (1); Shah, N.; Warrington, J.; Hudson, T. J. (1); Lander, E. (1)
CS (1) Whitehead Institute/MIT Center for Genome Research, Cambridge, MA USA
SO American Journal of Human Genetics, (Oct., 1999) Vol. 65, No. 4, pp. A27. Meeting Info.: 49th Annual Meeting of the American Society of Human Genetics San Francisco, California, USA October 19-23, 1999 The American Society of Human Genetics
. ISSN: 0002-9297.
DT Conference
LA English
CC Genetics and Cytogenetics - Animal *03506
Genetics and Cytogenetics - Human *03508
Biochemical Studies - General *10060
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
Muridae 86375
IT Major Concepts
Methods and Techniques; Molecular Genetics (Biochemistry and Molecular Biophysics)
IT Chemicals & Biochemicals
sequence tag site: screening; DNA: pooled sample; SNP [single nucleotide polymorphism]: allele frequency
IT Methods & Equipment
GeneChip probe array: genetic analytical method; PCR [polymerase chain reaction]: DNA amplification, analytical method, sequencing techniques, in-situ recombinant gene expression detection, DNA amplification method; SNP genotyping [single nucleotide polymorphism genotyping]: genetic analytical method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Slide
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Muridae: Rodentia, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae); mouse (Muridae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Nonhuman Mammals; Nonhuman Vertebrates; Primates; Rodents; Vertebrates

L50 ANSWER 25 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1999:499337 BIOSIS
DN PREV199900499337
TI Direct comparison of SAGE and **Genechip** on quantitative accuracy in the transcript profiling analysis.
AU Aburatani, H. (1); Ishii, M. (1); Hashimoto, S.; Tsutsumi, S. (1); Wada, Y. (1); Matsushima, K.; Kodama, T. (1)
CS (1) RCAST, Univ Tokyo, Tokyo Japan
SO American Journal of Human Genetics, (Oct., 1999) Vol. 65, No. 4, pp. A220. Meeting Info.: 49th Annual Meeting of the American Society of Human Genetics San Francisco, California, USA October 19-23, 1999 The American Society of Human Genetics
. ISSN: 0002-9297.
DT Conference
LA English
CC Genetics and Cytogenetics - Human *03508
Cytology and Cytochemistry - Human *02508
Biochemical Methods - General *10050
Anatomy and Histology, General and Comparative - Gross Anatomy *11102
Blood, Blood-Forming Organs and Body Fluids - General; Methods *15001
Biophysics - General Biophysical Studies *10502
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Genetics; Methods and Techniques
IT Parts, Structures, & Systems of Organisms
blood monocyte: blood and lymphatics; macrophage: blood and lymphatics, immune system
IT Methods & Equipment
serial analysis of gene expression [SAGE]: analytical method, genetic method, transcript profiling analysis, quantitative accuracy; **GeneChip**: analytical method, transcript profiling analysis, quantitative accuracy, genetic method
IT Miscellaneous Descriptors
transcript profiling analysis: quantitative accuracy; Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 26 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:497730 BIOSIS
DN PREV199900497730
TI High-**density microarray genechip** analysis of altered gene expression profiles in hepatocellular carcinoma.
AU Kaiser, Stephan (1); Anderson, W. French; Hwang, Jung-Joo
CS (1) Univ of Tuebingen, Tuebingen Germany
SO Hepatology, (Oct., 1999) Vol. 30, No. 4 PART 2, pp. 391A. Meeting Info.: 50th Annual Meeting and Postgraduate Courses of the American Association for the Study of Liver Diseases Dallas, Texas, USA November 5-9, 1999 American Association for the Study of Liver Diseases
. ISSN: 0270-9139.
DT Conference
LA English
CC Digestive System - General; Methods *14001
Cytology and Cytochemistry - Human *02508
Genetics and Cytogenetics - Human *03508
Neoplasms and Neoplastic Agents - General *24002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Hominidae 86215
IT Major Concepts
Digestive System (Ingestion and Assimilation); Molecular Genetics

(Biochemistry and Molecular Biophysics); Tumor Biology
IT Diseases
hepatocellular carcinoma: digestive system disease, neoplastic disease
IT Alternate Indexing
Carcinoma, Hepatocellular (MeSH)
IT Methods & Equipment
high-**density microarray GeneChip**
analysis: genetic method
IT Miscellaneous Descriptors
gene expression; Meeting Abstract
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): aged, middle age, patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 27 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1999:386173 BIOSIS
DN PREV199900386173
TI A comparative evaluation of HIV genotyping by DNA sequencing and GeneChipTM Technologies.
AU Wilson, J. (1); Bean, P.; Robins, T.; Graziano, F.; Persing, D. (1)
CS (1) Mayo Clinic, Rochester, MN USA
SO Clinical Chemistry, (June, 1999) Vol. 45, No. 6 PART 2, pp. A65-A66. Meeting Info.: 51st Annual Meeting of the American Association of Clinical Chemistry New Orleans, Louisiana, USA July 25-29, 1999 American Association of Clinical Chemistry
. ISSN: 0009-9147.
DT Conference
LA English
CC Genetics of Bacteria and Viruses *31500
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
Enzymes - General and Comparative Studies; Coenzymes *10802
Chemotherapy - General; Methods; Metabolism *38502
Virology - General; Methods *33502
Pharmacology - General *22002
General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals *00520
BC Retroviridae 02623
Hominidae 86215
IT Major Concepts
Molecular Genetics (Biochemistry and Molecular Biophysics); Pharmacology
IT Chemicals & Biochemicals
antiretroviral agents: antiviral activity, resistance; HIV protease gene [human immunodeficiency virus protease gene] (Retroviridae): **mutation**; HIV reverse transcriptase gene [human immunodeficiency virus reverse transcriptase gene] (Retroviridae): **mutation**
IT Methods & Equipment
DNA sequencing: genetic method; **GeneChip** system: genetic method
IT Miscellaneous Descriptors
Meeting Abstract; Meeting Poster
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
HIV [human immunodeficiency virus] (Hominidae, Retroviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Animals; Chordates; Humans; Mammals; Microorganisms; Primates; Vertebrates; Viruses

L50 ANSWER 28 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS

AN 1999:345125 BIOSIS
DN PREV199900345125
TI Rapid p53 sequence analysis in primary lung cancer using an oligonucleotide **probe array**.
AU Ahrendt, Steven A.; Halachmi, Sarel; Chow, John T.; Wu, Li; Halachmi, Naomi; Yang, Stephen C.; Wehage, Scott; Jen, Jin; Sidransky, David (1)
CS (1) Department of Otolaryngology-Head and Neck Surgery, Johns Hopkins School of Medicine, 720 Rutland Avenue, Baltimore, MD, 21287 USA
SO Proceedings of the National Academy of Sciences of the United States of America, (June 22, 1999) Vol. 96, No. 13, pp. 7382-7387. ISSN: 0027-8424.
DT Article
LA English
SL English
AB The p53 gene was sequenced in 100 primary human lung cancers by using direct dideoxynucleotide cycle sequencing and compared with sequence analysis by using the p53 **GeneChip** assay. Differences in sequence analysis between the two techniques were further evaluated to determine the accuracy and limitations of each method. p53 **mutations** were either detected by using both techniques or, if only detected by one technique, were confirmed by using **mutation** -specific oligonucleotide **hybridization**. Dideoxynucleotide sequencing of the conserved regions of the p53 gene (exons 5-9) detected 76% of the **mutations** within this region of the gene. The **GeneChip** p53 assay detected 81% of all (exons 2-11) **mutations**, including 80% of the **mutations** within the conserved regions of the gene. The **GeneChip** assay detected 46 of 52 missense **mutations** (88%), but 0 of 5 frameshift **mutations**. The specificity of direct sequencing and of the p53 **GeneChip** assay at detecting p53 **mutations** were 100% and 98%, respectively.The **GeneChip** p53 assay is a rapid and reasonably accurate approach for detecting p53 **mutations**; however, neither direct sequencing nor the p53 **GeneChip** are infallible at p53 **mutation** detection.
CC Genetics and Cytogenetics - General *03502
Biochemical Studies - General *10060
Biophysics - General Biophysical Studies *10502
Pathology, General and Miscellaneous - Diagnostic *12504
Respiratory System - General; Methods *16001
Neoplasms and Neoplastic Agents - General *24002
BC Hominidae 86215
IT Major Concepts
Genetics; Methods and Techniques; Oncology (Human Medicine, Medical Sciences)
IT Diseases
lung cancer: neoplastic disease, respiratory system disease
IT Chemicals & Biochemicals
dideoxynucleotide: sequencing; human p53 gene (Hominidae): **mutation**, sequence analysis, tumor-suppressor gene
IT Alternate Indexing
Lung Neoplasms (MeSH)
IT Methods & Equipment
p53 **GeneChip** assay: analytical method, oligonucleotide **probe** assay, detection method
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae): patient
ORGN Organism Superterms
Animals; Chordates; Humans; Mammals; Primates; Vertebrates

L50 ANSWER 29 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1998:356937 BIOSIS
DN PREV199800356937
TI Comparative performance of high-**density** oligonucleotide sequencing and dideoxynucleotide sequencing of HIV type 1 pol from

clinical samples.
AU Gunthard, Huldrych F. (1); Wong, Joseph K.; Ignacio, Caroline C.; Havlir, Diane V.; Richman, Douglas D.
CS (1) Dep. Pathol. and Med., Univ. California San Diego, 9500 Gilman Drive, La Jolla, CA 92093-0679 USA
SO AIDS Research and Human Retroviruses, (July 1, 1998) Vol. 14, No. 10, pp. 869-876.
ISSN: 0889-2229.
DT Article
LA English
AB The performance of the high-**density** oligonucleotide **array** methodology (**GeneChip**) in detecting drug resistance **mutations** in HIV-1 pol was compared with that of automated dideoxynucleotide sequencing (ABI) of clinical samples, viral stocks, and plasmid-derived NL4-3 clones. Sequences from 29 clinical samples (plasma RNA, n = 17; lymph node RNA, n = 5; lymph node DNA, n = 7) from 12 patients, from 6 viral stock RNA samples, and from 13 NL4-3 clones were generated by both methods. Editing was done independently by a different investigator for each method before comparing the sequences. In addition, NL4-3 wild type (WT) and **mutants** were mixed in varying concentrations and sequenced by both methods. Overall, a concordance of 99.1% was found for a total of 30,865 bases compared. The comparison of clinical samples (plasma RNA and lymph node RNA and DNA) showed a slightly lower match of base calls, 98.8% for 19,831 nucleotides compared (protease region, 99.5%, n = 8272; RT region, 98.3%, n = 11,316), than for viral stocks and NL4-3 clones (protease region, 99.8%; RT region, 99.5%). Artificial mixing experiments showed a bias toward calling wild-type bases by **GeneChip**. Discordant base calls are most likely due to differential detection of mixtures. The concordance between **GeneChip** and ABI was high and appeared dependent on the nature of the templates (directly amplified versus cloned) and the complexity of mixes.
CC Clinical Biochemistry; General Methods and Applications *10006
Biochemical Methods - Nucleic Acids, Purines and Pyrimidines *10052
Biophysics - Molecular Properties and Macromolecules *10506
Pathology, General and Miscellaneous - Diagnostic *12504
Genetics of Bacteria and Viruses *31500
Virology - Animal Host Viruses *33506
Medical and Clinical Microbiology - Virology *36006
Chemotherapy - Antiviral Agents *38506
BC Retroviridae 02623
IT Major Concepts
Clinical Chemistry (Allied Medical Sciences); Molecular Genetics (Biochemistry and Molecular Biophysics); Pharmacology
IT Parts, Structures, & Systems of Organisms
lymph node: blood and lymphatics, immune system; plasma: blood and lymphatics
IT Chemicals & Biochemicals
HIV type 1 pol [human immunodeficiency virus type 1 pol]: analysis
IT Methods & Equipment
dideoxynucleotide sequencing: diagnostic method, molecular genetic method; **GeneChip** high-**density** oligonucleotide sequencing: diagnostic method, molecular genetic method
IT Miscellaneous Descriptors
drug-resistance **mutations**
ORGN Super Taxa
Retroviridae: Animal Viruses, Viruses, Microorganisms
ORGN Organism Name
HIV type 1 [human immunodeficiency virus type 1] (Retroviridae): pathogen
ORGN Organism Superterms
Animal Viruses; Microorganisms; Viruses

L50 ANSWER 30 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1997:454044 BIOSIS
DN PREV199799753247

TI DNA on a chip: Serving up the **genome** for diagnostics and research.
AU Wallace, Robert W.
SO Molecular Medicine Today, (1997) Vol. 3, No. 9, pp. 384-389.
ISSN: 1357-4310.
DT Journal; Article
LA English
CC General Biology - Information, Documentation, Retrieval and Computer Applications *00530
Genetics and Cytogenetics - Human *03508
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Pathology, General and Miscellaneous - Diagnostic *12504
BC Hominidae *86215
IT Major Concepts
Genetics; Information Studies; Pathology
IT Miscellaneous Descriptors
COMPUTER APPLICATIONS; DIAGNOSTIC TECHNOLOGY; DNA; **GENECHIP**; GENETIC DISEASE SCREENING; GENETIC RESEARCH; **GENOME**; MOLECULAR GENETICS
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia
ORGN Organism Name
human (Hominidae)
ORGN Organism Superterms
animals; chordates; humans; mammals; primates; vertebrates

L50 ANSWER 31 OF 31 BIOSIS COPYRIGHT 2001 BIOSIS
AN 1996:402345 BIOSIS
DN PREV199699124701
TI Sequencing HIV isolates using the **GeneChip** HIV PRT assay.
AU Garrett, Miyada C. (1); Liang, V.; Tran, H. M.; Mittman, M.; Morris, M.; Kaplan, P.
CS (1) 3380 Central Expressway, Santa Clara, CA 95051 USA
SO ELEVENTH INTERNATIONAL CONFERENCE ON AIDS.. (1996) pp. 8. Eleventh International Conference on AIDS, Vol. One. One world: One hope.
Publisher: Eleventh International Conference on AIDS Vancouver, British Columbia, Canada.
Meeting Info.: Eleventh International Conference on AIDS, Vol. One. One world: One hope Vancouver, British Columbia, Canada July 7-12, 1996
DT Conference
LA English
CC General Biology - Symposia, Transactions and Proceedings of Conferences, Congresses, Review Annuals 00520
Biochemical Studies - Nucleic Acids, Purines and Pyrimidines 10062
Biochemical Studies - Proteins, Peptides and Amino Acids 10064
Biophysics - General Biophysical Techniques 10504
Enzymes - Chemical and Physical *10806
Enzymes - Physiological Studies *10808
Genetics of Bacteria and Viruses *31500
Immunology and Immunochemistry - Immunopathology, Tissue Immunology *34508
Medical and Clinical Microbiology - Virology *36006
BC Retroviridae 02623
Hominidae *86215
IT Major Concepts
Clinical Immunology (Human Medicine, Medical Sciences); Enzymology (Biochemistry and Molecular Biophysics); Genetics; Infection
IT Miscellaneous Descriptors
ANALYTICAL METHOD; MEETING ABSTRACT; PLASMID REVERSE TRANSCRIPTASE
ORGN Super Taxa
Hominidae: Primates, Mammalia, Vertebrata, Chordata, Animalia; Retroviridae: Viruses
ORGN Organism Name
human (Hominidae); human immunodeficiency virus (Retroviridae)
ORGN Organism Superterms
animals; chordates; humans; mammals; microorganisms; primates;

vertebrates; viruses

=> fil medline

FILE 'MEDLINE' ENTERED AT 12:39:19 ON 26 JAN 2001

FILE LAST UPDATED: 27 OCT 2000 (20001027/UP). FILE COVERS 1960 TO DATE.

MEDLINE thesauri in the /CN, /CT, and /MN fields incorporate the MeSH 2000 vocabulary. Enter HELP THESAURUS for details.

The OLDMEDLINE file segment now contains data from 1958 through 1965. Enter HELP CONTENT for details.

Left, right, and simultaneous left and right truncation are available in the Basic Index. See HELP SFIELDS for details.

THIS FILE CONTAINS CAS REGISTRY NUMBERS FOR EASY AND ACCURATE SUBSTANCE IDENTIFICATION.

MEDLINE UPDATES ARE ON HOLD UNTIL AFTER THE ANNUAL RELOAD HAS BEEN COMPLETED. NOTICE WILL BE GIVEN ONCE THE RELOAD IS COMPLETED AND RELOAD DETAILS WILL BE FOUND IN HELP RLOAD.

=> d all tot

L85 ANSWER 1 OF 37 MEDLINE
AN 2000471596 MEDLINE
DN 20423227
TI Housekeeping genes commanded to commit suicide in CpG-cleavage commitment upstream of Bcl-2 inhibition in caspase-dependent and -independent pathways.
AU Qi L; Sit K H
CS Department of Anatomy, Faculty of Medicine, National University of Singapore, Kent Ridge, 117597, Singapore.
SO Mol Cell Biol Res Commun, (2000 May) 3 (5) 319-27.
Journal code: DRR. ISSN: 1522-4724.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200012
EW 20001202
AB A CpG-specific commitment common to both caspase-dependent and -independent cell deaths implies critical gene activity from epigenetic modulation. Using a focused microarray (**genechip**) of 22 housekeeping genes, which have canonical CpG islands at 5'-promoter regions, here we show critical regulation of vital intermediary metabolism and cell structure that are common to both caspase-dependent fasL-mediated and caspase-independent etoposide-mediated cell deaths. Gene activity of at least twofold under or over control levels and common to both cell death pathways was considered to be significantly regulated in common. Seven genes controlling energy production in glycolysis, tricarboxylic acid cycle, and the respiratory electron transport chain were significantly downregulated in common. Energy depletion is lethal. Downregulated pyruvate dehydrogenase E1 gene, in addition, suggested primary metabolic acidification. Cell acidification is also lethal. Critical derangement of the cell structure was suggested by common downregulation of the basal histone gene H2A.X which is required for nucleosome assembly. Common upregulation of the alpha-tubulin gene suggested perturbation of vital microtubular dynamics. Gene-commanded cell suicide was suggested. We further show that a Bcl-2 overexpression of three- to fourfold above normal levels could not prevent the CpG-specific megabase DNA cleavages in the two cell death pathways, but abolished their

low-molecular-weight 200-bp ladder cleavages. Together with incomplete suppression of the other apoptotic expressions, the Bcl-2 inhibition point appeared downstream from the CpG-cleavage commitment point. Copyright 2000 Academic Press.

CT Check Tags: Human; Support, Non-U.S. Gov't
Annexin V: ME, metabolism
Apoptosis: DE, drug effects
*Apoptosis: GE, genetics
Caspases: GE, genetics
*Caspases: ME, metabolism
Cell Cycle
*Cell Death: GE, genetics
Cell Line
*CpG Islands: GE, genetics
DNA Fragmentation
Electrophoresis, Gel, Pulsed-Field
Energy Metabolism: GE, genetics
Etoposide: PD, pharmacology
*Gene Expression Regulation
*Genes, bcl-2: GE, genetics
Membrane Glycoproteins: PD, pharmacology
Oligonucleotide Array Sequence Analysis
Tumor Cells, Cultured

RN 33419-42-0 (Etoposide)

CN 0 (Annexin V); 0 (FasL protein); 0 (Membrane Glycoproteins); EC 3.4.22.- (Caspases)

L85 ANSWER 2 OF 37 MEDLINE

AN 2000456127 MEDLINE

DN 20296937

TI Genome-directed primers for selective labeling of bacterial transcripts for DNA **microarray** analysis.

AU Talaat A M; Hunter P; Johnston S A

CS Center for Biomedical Inventions and Department of Medicine, University of Texas-Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas TX 75390-8573, USA.

SO NATURE BIOTECHNOLOGY, (2000 Jun) 18 (6) 679-82.
Journal code: CQ3. ISSN: 1087-0156.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

EM 200012

EW 20001201

AB DNA **microarrays** have the ability to analyze the expression of thousands of the same set of genes under at least two different experimental conditions. However, DNA **microarrays** require substantial amounts of RNA to generate the probes, especially when bacterial RNA is used for hybridization (50 microg of bacterial total RNA contains approximately 2 microg of mRNA). We have developed a computer-based algorithm for prediction of the minimal number of primers to specifically anneal to all genes in a given genome. The algorithm predicts, for example, that 37 oligonucleotides should prime all genes in the Mycobacterium tuberculosis genome. We tested the usefulness of the genome-directed primers (GDPs) in comparison to random primers for gene expression profiling using DNA **microarrays**. Both types of primers were used to generate fluorescent-labeled probes and to hybridize to an **array** of 960 mycobacterial genes. Compared to random-primer probes, the GDP probes were more sensitive and more specific, especially when mammalian RNA samples were spiked with mycobacterial RNA. The GDPs were used for gene expression profiling of mycobacterial cultures grown to early log or stationary growth phases. This approach could be useful for accurate genome-wide expression analysis, especially for in vivo gene expression profiling, as well as directed amplification of **sequenced** genomes.

CT **Algorithms**

Base Sequence
*DNA Primers
*DNA, Bacterial
***Genome, Bacterial**
Molecular Sequence Data
Mycobacterium tuberculosis: GE, genetics
Nucleic Acid Hybridization
***Oligonucleotide Array Sequence Analysis: MT, methods**
RNA, Bacterial
Software
Transcription, Genetic
CN 0 (DNA Primers); 0 (DNA, Bacterial); 0 (RNA, Bacterial)

L85 ANSWER 3 OF 37 MEDLINE
AN 2000437445 MEDLINE
DN 20381133
TI Comparative evaluation of three human immunodeficiency virus genotyping systems: the HIV-GenotypR method, the HIV PRT **GeneChip** assay, and the HIV-1 RT line probe assay.
AU Wilson J W; Bean P; Robins T; Graziano F; Persing D H
CS Division of Infectious Diseases, Department of Internal Medicine, Mayo Clinic, Rochester, Minnesota 55905, USA.. wilson.john@mayo.edu
SO JOURNAL OF CLINICAL MICROBIOLOGY, (2000 Aug) 38 (8) 3022-8.
Journal code: HSH. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
EW 20001104
AB Evaluation of drug resistance by human immunodeficiency virus (HIV) genotyping has proven to be useful for the selection of drug combinations with maximum antiretroviral activity. We compared three genotyping methods for identification of mutations known to confer drug resistance in the reverse transcriptase (RT) and protease genes of HIV type 1 (HIV-1). The HIV-GenotypR method (GenotypR; Specialty Laboratories, Inc., Santa Monica, Calif.) with the ABI 377 DNA sequencer (Applied Biosystems Inc.), the HIV PRT **GeneChip** assay (**GeneChip**; Affymetrix, Santa Clara, Calif.), and the HIV-1 RT Line Probe Assay (LiPA; Innogenetics, Alpharetta, Ga.) were used to genotype plasma samples from HIV-infected patients attending the University of Wisconsin Hospitals and Clinics and the Mayo Clinic. At the time of analysis, patients were failing combination therapy (n = 18) or were treatment naive (n = 6). Forty codons of the RT and protease genes were analyzed by GenotypR and **GeneChip** for resistance-associated mutations. LiPA analyzed seven RT codons for mutations. Each sample was genotyped by all three assays, and each assay was subjected to pairwise comparisons. At least 92% of the codons tested (by the three assays) in paired comparisons were concordant. GenotypR and **GeneChip** demonstrated 96.6% concordance over the 40 codons tested. GenotypR identified slightly more mutations than **GeneChip** and LiPA; **GeneChip** identified all primary mutations that corresponded to failing treatment regimens. Each assay identified at least 84% of the mutations identified by the other assays. Mutations that were discordant between the assays mainly comprised secondary mutations and natural polymorphisms. The assays had better concordance for mutations that corresponded to current failing regimens, present in the more predominant viral quasispecies. In the treatment-naive patients, GenotypR, **GeneChip**, and LiPA mainly identified wild-type virus. Only the LiPA identified K70R, a possible transmitted zidovudine resistance mutation, in the RT gene of a treatment-naive patient. We conclude that although discrepancies in results exist between assays, each assay showed a similar capacity to identify potentially clinically relevant mutations related to patient treatment regimens.
CT Check Tags: Comparative Study; Human
Anti-HIV Agents: PD, pharmacology
Anti-HIV Agents: TU, therapeutic use

Codon: GE, genetics
Drug Resistance, Microbial: GE, genetics
Evaluation Studies
Genotype
HIV Infections: DT, drug therapy
*HIV Infections: VI, virology
*HIV Protease: GE, genetics
*HIV-1: CL, classification
HIV-1: DE, drug effects
HIV-1: EN, enzymology
*HIV-1: GE, genetics
*HIV-1 Reverse Transcriptase: GE, genetics
Mutation
Oligonucleotide Array Sequence Analysis: MT, methods
Oligonucleotide Probes
Reagent Kits, Diagnostic
Reverse Transcriptase Inhibitors: PD, pharmacology
Reverse Transcriptase Inhibitors: TU, therapeutic use
RNA, Viral: AN, analysis
Sequence Analysis, DNA: MT, methods

CN EC 2.7.7.- (HIV-1 Reverse Transcriptase); EC 3.4.23.- (HIV Protease); 0 (Anti-HIV Agents); 0 (Codon); 0 (Oligonucleotide Probes); 0 (Reagent Kits, Diagnostic); 0 (Reverse Transcriptase Inhibitors); 0 (RNA, Viral)

L85 ANSWER 4 OF 37 MEDLINE
AN 2000425955 MEDLINE
DN 20416146
TI Detection of aberrations of 17p and p53 gene in gastrointestinal cancers by dual (two-color) fluorescence in situ hybridization and **GeneChip** p53 assay.
AU Takahashi Y; Nagata T; Asai S; Shintaku K; Eguchi T; Ishii Y; Fujii M; Ishikawa K
CS Department of Pharmacology, Nihon University School of Medicine, Tokyo, Japan.
SO CANCER GENETICS AND CYTOGENETICS, (2000 Aug) 121 (1) 38-43.
Journal code: CMT. ISSN: 0165-4608.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200011
EW 20001103
AB We performed dual (two-color) fluorescence in situ hybridization (FISH) using direct fluorescent labeling probes for p53 and chromosome 17 in six gastrointestinal (3 stomach and 3 colon) cancers. In three of these (1 stomach and 2 colon) the interphase cell nuclei showed an imbalance of signals for the p53 and chromosome 17; that is, the p53 signal count was lower than the chromosome 17 signal count, indicating deletion of the p53 gene. Moreover, metaphase FISH analysis demonstrated that those nuclei actually had a chromosome 17 with deletion of the p53 gene. Interestingly, these three cases had an abnormal chromosome 17 copy number, that is, chromosome 17 aneusomy. Furthermore, to investigate the possibility of p53 mutation in tumors with an imbalance of signals for chromosome 17 and p53 per nucleus, we performed a **GeneChip** p53 assay which has recently been developed. **GeneChip** p53 assay demonstrated that a primary tumor sample from one colon cancer case had a heterozygous point mutation of CGT (Arg) to CAT (His) at codon 273 in exon 8. In addition, a sample of metastatic tumor in the liver from the same case revealed two heterozygous point mutations. One of them was the same mutation as that is the primary tumor; the other was GTG (Val) to GGG (Gly) at codon 217 in exon 6. In conclusion, we found that the combination of dual-color FISH and **GeneChip** p53 assay offered reliable results and important information concerning not only deletion of the p53 gene and chromosome 17 aneusomy but also p53 mutations. Using these techniques, we demonstrated that an imbalance of signals for chromosome 17 and p53 per nucleus, chromosome 17 aneusomy, and accumulation of p53 mutations had occurred

during carcinogenesis and development of gastrointestinal cancers.
CT Check Tags: Human; Support, Non-U.S. Gov't
Centromere
*Chromosome Aberrations: GE, genetics
*Chromosomes, Human, Pair 17: GE, genetics
*Colonic Neoplasms: GE, genetics
Fluorescent Dyes
Gene Dosage
*Genes, p53: GE, genetics
In Situ Hybridization, Fluorescence: MT, methods
Oligonucleotide Array Sequence Analysis: MT, methods
Point Mutation
*Stomach Neoplasms: GE, genetics
CN 0 (Fluorescent Dyes)

L85 ANSWER 5 OF 37 MEDLINE
AN 2000322578 MEDLINE
DN 20322578
TI Genomics, gene expression and DNA **arrays**.
AU Lockhart D J; Winzeler E A
CS Genomics Institute of the Novartis Research Foundation, San Diego, California 92121, USA.
SO NATURE, (2000 Jun 15) 405 (6788) 827-36. Ref: 109
Journal code: NSC. ISSN: 0028-0836.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, ACADEMIC)
LA English
FS Priority Journals; Cancer Journals
EM 200009
EW 20000903
AB Experimental genomics in combination with the growing body of **sequence** information promise to revolutionize the way cells and cellular processes are studied. Information on genomic **sequence** can be used experimentally with high-density DNA **arrays** that allow complex mixtures of RNA and DNA to be interrogated in a parallel and quantitative fashion. DNA **arrays** can be used for many different purposes, most prominently to measure levels of gene expression (messenger RNA abundance) for tens of thousands of genes simultaneously. Measurements of gene expression and other applications of **arrays** embody much of what is implied by the term 'genomics'; they are broad in scope, large in scale, and take advantage of all available **sequence** information for experimental design and data interpretation in pursuit of biological understanding.
CT Check Tags: Animal; Human
Data Interpretation, Statistical
*DNA
***Gene Expression**
Gene Expression Profiling
Gene Expression Regulation
Genes: PH, physiology
***Genome**
***Oligonucleotide Array Sequence Analysis**
RNA
RN 63231-63-0 (RNA); 9007-49-2 (DNA)

L85 ANSWER 6 OF 37 MEDLINE
AN 2000311505 MEDLINE
DN 20311505
TI Monitoring gene expression using DNA microarrays.
AU Harrington C A; **Rosenow C**; Retief J
CS Affymetrix, Inc., Santa Clara, 95051, USA.. chris_harrington@affymetrix.com
SO Curr Opin Microbiol, (2000 Jun) 3 (3) 285-91. Ref: 41
Journal code: DAY. ISSN: 1369-5274.

CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200010
EW 20001001
AB The concurrent development of high-density array technologies and the complete sequencing of a number of microbial genomes is providing the opportunity to comprehensively and efficiently survey the transcription profile of microorganisms under different conditions and well-defined genotypes. Microarray-based studies are uncovering broad patterns of genetic activity, providing new understanding of gene functions and, in some cases, generating unexpected insight into transcriptional processes and biological mechanisms. One topic that has come to the forefront is how best to effectively manage and interpret the large data sets being generated. Although progress has been made, this remains a challenging opportunity for functional genomics research.
CT Gene Expression Regulation, Bacterial
Gene Expression Regulation, Fungal
Gene Expression Regulation, Viral
*Molecular Biology: TD, trends
***Oligonucleotide Array Sequence Analysis: MT, methods**

L85 ANSWER 7 OF 37 MEDLINE
AN 2000294875 MEDLINE
DN 20294875
TI Determination of genes involved in the process of implantation: application of **GeneChip** to scan 6500 genes.
AU Yoshioka K; Matsuda F; Takakura K; Noda Y; Imakawa K; Sakai S
CS Laboratory of Animal Breeding, University of Tokyo, Japan.
SO BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, (2000 Jun 7) 272 (2) 531-8.
Journal code: 9Y8. ISSN: 0006-291X.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 200009
EW 20000903
AB Using the high-density arrays of oligonucleotides (**GeneChip**) technology, the expression of uterine genes was examined before and after conceptus implantation in mice. Of the 6500 genes analyzed, levels of 399 gene expressions changed; 192 genes increased levels of expression while the remaining 207 genes declined. The findings suggest that both gene activation and deactivation (suppression) are required for successful implantation. Copyright 2000 Academic Press.
CT Check Tags: Animal; Female; Support, Non-U.S. Gov't
Down-Regulation (Physiology)
*Gene Expression Profiling
Genes: GE, genetics
Mice
***Oligonucleotide Array Sequence Analysis**
*Postimplantation Phase: GE, genetics
Pregnancy
*Preimplantation Phase: GE, genetics
Reproducibility of Results
Reverse Transcriptase Polymerase Chain Reaction
RNA, Messenger: GE, genetics
RNA, Messenger: ME, metabolism
Up-Regulation (Physiology)
*Uterus: ME, metabolism
CN 0 (RNA, Messenger)

L85 ANSWER 8 OF 37 MEDLINE

AN 2000283293 MEDLINE
DN 20283293
TI Comparison of TP53 mutations identified by oligonucleotide microarray and conventional DNA sequence analysis.
AU Wen W H; Bernstein L; Lescallett J; Beazer-Barclay Y; Sullivan-Halley J; White M; Press M F
CS Department of Pathology, University of Southern California School of Medicine, Los Angeles 90033, USA.
NC CA48780 (NCI)
CA50589 (NCI)
SO CANCER RESEARCH, (2000 May 15) 60 (10) 2716-22.
Journal code: CNF. ISSN: 0008-5472.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 200008
EW 20000803
AB As the rate of gene discovery accelerates, more efficient methods are needed to analyze genes in human tissues. To assess the efficiency, sensitivity, and specificity of different methods, alterations of TP53 were independently evaluated in 108 ovarian tumors by conventional DNA sequence analysis and oligonucleotide microarray (p53 **GeneChip**). All mutations identified by oligonucleotide microarray and all disagreements with conventional gel-based DNA sequence analysis were confirmed by re-analysis with manual and automated dideoxy DNA sequencing. A total of 77 ovarian cancers were identified as having TP53 mutations by one of the two approaches, 71 by microarray and 63 by gel-based DNA sequence analysis. The same mutation was identified in 57 ovarian cancers, and the same wild type TP53 sequence was observed in 31 ovarian cancers by both methods, for a concordance rate of 81%. Among the mutation analyses discordant by these methods for TP53 sequence were 14 cases identified as mutated by microarray but not by conventional DNA sequence analysis and 6 cases identified as mutated by conventional DNA sequence analysis but not by microarray. Overall, the oligonucleotide microarray demonstrated a 94% accuracy rate, a 92% sensitivity, and an 100% specificity. Conventional DNA sequence analysis demonstrated an 87% accuracy rate, 82% sensitivity, and a 100% specificity. Patients with TP53 mutations had significantly shorter overall survival than those with no mutation (P = 0.02). Women with mutations in loop2, loop3, or the loop-sheet-helix domain had shorter survival than women with other mutations or women with no mutations (P = 0.01). Although further refinement would be helpful to improve the detection of certain types of TPS3 alterations, oligonucleotide microarrays were shown to be a powerful and effective tool for TP53 mutation detection.
CT Check Tags: Comparative Study; Female; Human; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
*Genes, p53: GE, genetics
*Mutation
***Oligonucleotide Array Sequence Analysis**
Ovarian Neoplasms: GE, genetics
Ovarian Neoplasms: MO, mortality
Polymorphism, Single-Stranded Conformational
***Sequence Analysis, DNA**
Survival Rate

L85 ANSWER 9 OF 37 MEDLINE
AN 2000251004 MEDLINE
DN 20251004
TI Technical assessment of the affymetrix yeast expression **GeneChip** YE6100 platform in a heterologous model of genes that confer resistance to antimalarial drugs in yeast.
AU Nau M E; Emerson L R; Martin R K; Kyle D E; Wirth D F; Vahey M
CS Henry M. Jackson Foundation for the Advancement of Military Medicine, Rockville, Maryland, USA.
SO JOURNAL OF CLINICAL MICROBIOLOGY, (2000 May) 38 (5) 1901-8.

Journal code: HSH. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200008
EW 20000804
AB The advent of high-density gene array technology has revolutionized approaches to drug design, development, and characterization. At the laboratory level, the efficient, consistent, and dependable exploitation of this complex technology requires the stringent standardization of protocols and data analysis platforms. The Affymetrix YE6100 expression **GeneChip** platform was evaluated for its performance in the analysis of both global (6,000 yeast genes) and targeted (three pleiotropic multidrug resistance genes of the ATP binding cassette transporter family) gene expression in a heterologous yeast model system in the presence and absence of the antimalarial drug chloroquine. Critical to the generation of consistent data from this platform are issues involving the preparation of the specimen, use of appropriate controls, accurate assessment of experiment variance, strict adherence to optimized enzymatic and hybridization protocols, and use of sophisticated bioinformatics tools for data analysis.
CT Check Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
Algorithms
*Antimalarials: PD, pharmacology
ABC Transporters: GE, genetics
*Chloroquine: PD, pharmacology
*Drug Resistance, Microbial: GE, genetics
Drug Resistance, Multiple: GE, genetics
***Oligonucleotide Array Sequence Analysis: IS, instrumentation**
Oligonucleotide Array Sequence Analysis: MT, methods
RNA, Messenger: GE, genetics
Saccharomyces cerevisiae: DE, drug effects
*Saccharomyces cerevisiae: GE, genetics
RN 54-05-7 (Chloroquine)
CN 0 (Antimalarials); 0 (ABC Transporters); 0 (RNA, Messenger)

L85 ANSWER 10 OF 37 MEDLINE
AN 2000223579 MEDLINE
DN 20223579
TI Comprehensive gene expression profile of the adult human renal cortex: analysis by cDNA **array** hybridization.
AU Yano N; Endoh M; Fadden K; Yamashita H; Kane A; Sakai H; Rifai A
CS Department of Pathology, Rhode Island Hospital and Brown University School of Medicine, Providence, RI 02903, USA.
NC DK49361 (NIDDK)
SO KIDNEY INTERNATIONAL, (2000 Apr) 57 (4) 1452-9.
Journal code: KVB. ISSN: 0085-2538.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
EW 20000702
AB BACKGROUND: Profiling of gene expression in healthy and diseased renal tissue is important for elucidating the pathogenesis of renal diseases. Comprehensive information about the genes expressed in renal tissue is unavailable. The recently developed cDNA **array** hybridization methodology allows simultaneous monitoring of thousands of genes expressed renal tissue. METHODS: Complex [alpha-33P]-labeled cDNA probes were prepared from histopathologically uninvolved remnants of nine renal tissues obtained by nephrectomy. Each probe was hybridized to a high-density **array** of 18,326 paired target genes. The radioactive hybridization signals by phosphorimager screens were quantitated by special **software**. Bioinformatics from public genomic databases were used to assign a chromosomal location of each

expressed transcript and gene function. Cluster analysis was used to arrange genes according to the similarity in pattern of gene expression. RESULTS: A total of 7563 different gene transcripts was detected in the nine tissue samples. Approximately 870 of these genes were full-length mRNA human transcripts (HT), and the remaining 6693 were expressed **sequence** tags (ESTs). The full-length transcripts were classified by function of the gene product and were listed with information of their chromosomal positions. To allow a comparison between gene expression in clinical and experimental studies, the mouse genes with known similar function to the human counterpart were included in the bioinformatics analysis. Cluster analysis of 502 full-length genes that are expressed in four or more renal tissues revealed more than 110 genes that are highly expressed in all the renal specimens. CONCLUSIONS: The presented data constitute a comprehensive preliminary transcriptional map of the adult human renal cortex. The information may serve as a resource for speeding up the discovery of genes underlying human renal disease. The integrated listing of the full-length expressed human and mouse genes is available through e-mail (Abdalla_Rifai@Brown.edu).

CT Check Tags: Animal; Female; Human; Male; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Adult
Aged
Chromosome Mapping
Cluster Analysis
Data Display
DNA, Complementary: GE, genetics
***Gene Expression**
Genome
Kidney: PH, physiology
*Kidney Cortex: PH, physiology
Mice: GE, genetics
Middle Age
Nucleic Acid Hybridization
Oligonucleotide Array Sequence Analysis

CN 0 (DNA, Complementary)

L85 ANSWER 11 OF 37 MEDLINE
AN 2000206561 MEDLINE
DN 20206561
TI Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse.
AU Lindblad-Toh K; Winchester E; Daly M J; Wang D G; Hirschhorn J N; Laviolette J P; Ardlie K; Reich D E; Robinson E; Sklar P; Shah N; Thomas D; Fan J B; **Gingeras T**; Warrington J; Patil N; Hudson T J; Lander E S
CS Whitehead Institute/MIT Center for Genome Research, Whitehead Institute for Biomedical Research, Cambridge, MA, USA.. kersli@genome.wi.mit.edu
NC HG01806 (NHGRI)
SO NATURE GENETICS, (2000 Apr) 24 (4) 381-6.
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 200007
EW 20000701
AB Single-nucleotide polymorphisms (SNPs) have been the focus of much attention in human genetics because they are extremely abundant and well-suited for automated large-scale genotyping. Human SNPs, however, are less informative than other types of genetic markers (such as simple-sequence length polymorphisms or microsatellites) and thus more loci are required for mapping traits. SNPs offer similar advantages for experimental genetic organisms such as the mouse, but they entail no loss of informativeness because bi-allelic markers are fully informative in analysing crosses between inbred strains. Here we report a large-scale analysis of SNPs in the mouse genome. We characterized the rate of

nucleotide polymorphism in eight mouse strains and identified a collection of 2,848 SNPs located in 1,755 sequence-tagged sites (STSs) using high-density oligonucleotide arrays. Three-quarters of these SNPs have been mapped on the mouse genome, providing a first-generation SNP map of the mouse. We have also developed a multiplex genotyping procedure by which a genome scan can be performed with only six genotyping reactions per animal.

CT Check Tags: Animal; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
CpG Islands
Gene Frequency
Genome
Genotype
Mice
*Mice, Inbred Strains: GE, genetics
Oligonucleotide Array Sequence Analysis
Phylogeny
Physical Chromosome Mapping
*Point Mutation: GE, genetics
*Polymorphism (Genetics): GE, genetics
Sequence Tagged Sites

L85 ANSWER 12 OF 37 MEDLINE
AN 2000179482 MEDLINE
DN 20179482
TI Genomic-scale gene expression profiling of normal and malignant immune cells.
AU Alizadeh A A; Staudt L M
CS Department of Biochemistry, M309 Genetics, Alway Building, Stanford University School of Medicine, Stanford, CA 94305, USA.
SO CURRENT OPINION IN IMMUNOLOGY, (2000 Apr) 12 (2) 219-25. Ref: 27
Journal code: AH1. ISSN: 0952-7915.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 200007
EW 20000704
AB Gene expression variation is critical for the normal development and physiology of immune cells. Using cDNA **microarrays**, a systematic, genomic-scale view of gene expression in immune cells at many stages of differentiation and activation can be obtained. From the high vantagepoint provided by this technology, the gene expression physiology of immune cells appears remarkably ordered and logical. Each stage of lymphocyte differentiation can be defined by a characteristic gene expression signature. Genes that are co-regulated over hundreds of experimental conditions often encode functionally related proteins. Gene expression profiles also provide unprecedented ability to define the molecular and functional relationships between normal and malignant lymphocyte cell populations.
CT Check Tags: Animal; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Algorithms
Antigens, Differentiation, B-Lymphocyte: BI, biosynthesis
Antigens, Differentiation, B-Lymphocyte: GE, genetics
Antigens, Neoplasm: BI, biosynthesis
Antigens, Neoplasm: GE, genetics
Antigens, Neoplasm: IM, immunology
B-Lymphocytes: IM, immunology
B-Lymphocytes: ME, metabolism
B-Lymphocytes: PA, pathology
Cell Differentiation: GE, genetics
Cell Line, Transformed
*Gene Expression Profiling
*Gene Expression Regulation, Neoplastic

Genetic Markers
*Genome
Germinal Center: CY, cytology
Lymphocyte Subsets: ME, metabolism
Lymphocyte Transformation
Neoplasms: GE, genetics
Neoplasms: IM, immunology
Neoplasms, Experimental: GE, genetics
Neoplasms, Experimental: IM, immunology
*Oligonucleotide Array Sequence Analysis
RNA, Messenger: BI, biosynthesis
RNA, Messenger: GE, genetics
RNA, Neoplasm: BI, biosynthesis
RNA, Neoplasm: GE, genetics
Transcription, Genetic
Tumor Cells, Cultured
Tumor Stem Cells: IM, immunology
Tumor Stem Cells: ME, metabolism
Tumor Stem Cells: PA, pathology
CN 0 (Antigens, Differentiation, B-Lymphocyte); 0 (Antigens, Neoplasm); 0 (Genetic Markers); 0 (RNA, Messenger); 0 (RNA, Neoplasm)

L85 ANSWER 13 OF 37 MEDLINE
AN 1999403426 MEDLINE
DN 99403426
TI **High-density** nucleoside analog probe arrays for enhanced hybridization.
AU Fidanza J A; McGall G H
CS Affymetrix, Inc., Santa Clara, CA 95051, USA.
SO NUCLEOSIDES AND NUCLEOTIDES, (1999 Jun-Jul) 18 (6-7) 1293-5.
Journal code: C5G. ISSN: 0732-8311.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199912
EW 19991201
AB DNA probe arrays were synthesized with analogs of 2,6-diaminopurine and 2'-O-methyl-thymidine in place of A and T. AT-rich **GeneChip** test arrays containing 14-mer or 20-mer analog probes improved hybridization to fluorescently-labeled RNA sequences under stringent conditions.
CT Indicators and Reagents
*Nucleic Acid Hybridization
*Oligonucleotide Probes
CN 0 (Indicators and Reagents); 0 (Oligonucleotide Probes)

L85 ANSWER 14 OF 37 MEDLINE
AN 1999362811 MEDLINE
DN 99362811
TI Mapping regulatory networks in microbial cells [see comments].
CM Comment in: Trends Microbiol 1999 Oct;7(10):398-9
AU VanBogelen R A; Greis K D; Blumenthal R M; Tani T H; Matthews R G
CS Parke-Davis Pharmaceutical Research Division, Warner-Lambert, Ann Arbor, MI 48105, USA.
NC GM08353 (NIGMS)
SO TRENDS IN MICROBIOLOGY, (1999 Aug) 7 (8) 320-8. Ref: 29
Journal code: B1N. ISSN: 0966-842X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199912
AB Genome **sequences** are the blueprints of diverse life forms but they reveal little information about how cells make coherent responses to

environmental changes. The combined use of gene fusions, gene chips, 2-D polyacrylamide gel electrophoresis, mass spectrometry and 'old-fashioned' microbial physiology will provide the means to reveal a cell's regulatory networks and how those networks are integrated.
CT Check Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
*Bacteria: GE, genetics
*Bacteria: ME, metabolism
*Computational Biology: MT, methods
Databases, Factual
Electrophoresis, Gel, Two-Dimensional
*Gene Expression Regulation, Bacterial
Genome, Bacterial
Oligonucleotide Array Sequence Analysis
Spectrum Analysis, Mass: MT, methods
Transcription, Genetic
Translation, Genetic

L85 ANSWER 15 OF 37 MEDLINE
AN 1999335531 MEDLINE
DN 99335531
TI Performance of the Affymetrix **GeneChip** HIV PRT 440 platform for antiretroviral drug resistance genotyping of human immunodeficiency virus type 1 clades and viral isolates with length polymorphisms.
AU Vahey M; Nau M E; Barrick S; Cooley J D; Sawyer R; Sleeker A A; Vickerman P; Bloor S; Larder B; Michael N L; Wegner S A
CS Division of Retrovirology, Walter Reed Army Institute of Research, Rockville, Maryland 20850, USA.. mvahey@pasteur.hjf.org
SO JOURNAL OF CLINICAL MICROBIOLOGY, (1999 Aug) 37 (8) 2533-7.
Journal code: HSH. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199910
EW 19991002
AB The performance of a silica chip-based resequencing method, the Affymetrix HIV PRT 440 assay (hereafter referred to as the Affymetrix assay), was evaluated on a panel of well-characterized nonclade B viral isolates and on isolates exhibiting length polymorphisms. Sequencing of human immunodeficiency virus type 1 (HIV-1) pol cDNAs from clades A, C, D, E, and F resulted in clade-specific regions of base-calling ambiguities in regions not known to be associated with resistance polymorphisms, as well as a small number of spurious resistance polymorphisms. The Affymetrix assay failed to detect the presence of additional serine codons distal to reverse transcriptase (RT) codon 68 that are associated with multinucleoside RT inhibitor resistance. The increasing prevalence of non-clade B HIV-1 strains in the United States and Europe and the identification of clinically relevant pol gene length polymorphisms will impact the generalizability of the Affymetrix assay, emphasizing the need to accommodate this expanding pool of pol genotypes in future assay versions.
CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.
*Acquired Immunodeficiency Syndrome: VI, virology
*Biological Assay: MT, methods
*Drug Resistance, Microbial: GE, genetics
*Genome, Viral
HIV-1: DE, drug effects
*HIV-1: GE, genetics
Microbiological Techniques
Polymorphism, Restriction Fragment Length
RNA, Viral: AN, analysis
RNA, Viral: GE, genetics
CN 0 (RNA, Viral)

L85 ANSWER 16 OF 37 MEDLINE

AN 1999307418 MEDLINE
DN 99307418
TI Rapid p53 sequence analysis in primary lung cancer using an oligonucleotide probe array.
AU Ahrendt S A; Halachmi S; Chow J T; Wu L; Halachmi N; Yang S C; Wehage S; Jen J; Sidransky D
CS Department of Surgery, Medical College of Wisconsin, 9200 West Wisconsin Avenue, Milwaukee, WI 53226, USA.
NC CA 58184-02 (NCI)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1999 Jun 22) 96 (13) 7382-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199909
EW 19990904
AB The p53 gene was sequenced in 100 primary human lung cancers by using direct dideoxynucleotide cycle sequencing and compared with sequence analysis by using the p53 **GeneChip** assay. Differences in sequence analysis between the two techniques were further evaluated to determine the accuracy and limitations of each method. p53 mutations were either detected by using both techniques or, if only detected by one technique, were confirmed by using mutation-specific oligonucleotide hybridization. Dideoxynucleotide sequencing of the conserved regions of the p53 gene (exons 5-9) detected 76% of the mutations within this region of the gene. The **GeneChip** p53 assay detected 81% of all (exons 2-11) mutations, including 80% of the mutations within the conserved regions of the gene. The **GeneChip** assay detected 46 of 52 missense mutations (88%), but 0 of 5 frameshift mutations. The specificity of direct sequencing and of the p53 **GeneChip** assay at detecting p53 mutations were 100% and 98%, respectively. The **GeneChip** p53 assay is a rapid and reasonably accurate approach for detecting p53 mutations; however, neither direct sequencing nor the p53 **GeneChip** are infallible at p53 mutation detection.
CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
*Lung Neoplasms: GE, genetics
Mutation
*Oligonucleotide Probes
*Protein p53: GE, genetics
***Sequence Analysis: MT, methods**
CN 0 (Oligonucleotide Probes); 0 (Protein p53)

L85 ANSWER 17 OF 37 MEDLINE
AN 1999187565 MEDLINE
DN 99187565
TI The maturation of nucleic acid technologies.
AU Freeman W M; Gioia L
CS Department of Physiology and Pharmacology, Wake Forest University School of Medicine, Winston-Salem, NC, USA.. wfreeman@medcenter.wpmail.wfu.edu
SO TRENDS IN BIOTECHNOLOGY, (1999 Feb) 17 (2) 44-5.
Journal code: ALJ. ISSN: 0167-7799.
CY ENGLAND: United Kingdom
DT Conference; Conference Article; (CONGRESSES)
Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199906
EW 19990602
CT Check Tags: Human
*Biotechnology: MT, methods
Biotechnology: TD, trends
Databases, Factual
DNA Probes
Gene Amplification: MT, methods

Gene Expression
*Genetic Techniques
Genome, Human
In Situ Hybridization: MT, methods
Neoplasms: DI, diagnosis
Neoplasms: GE, genetics
*Nucleic Acids
Peptide Nucleic Acids
Polymerase Chain Reaction
Sequence Analysis, DNA
CN 0 (DNA Probes); 0 (Nucleic Acids); 0 (Peptide Nucleic Acids)

L85 ANSWER 18 OF 37 MEDLINE
AN 1999112705 MEDLINE
DN 99112705
TI The genetics of cancer--a 3D model.
AU Cole K A; Krizman D B; Emmert-Buck M R
CS Pathogenetics Unit, Laboratory of Pathology, National Cancer Institute, Bethesda, Maryland 20892, USA.
SO NATURE GENETICS, (1999 Jan) 21 (1 Suppl) 38-41. Ref: 47
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199903
EW 19990305
AB Gene expression **microarrays** hold great promise for studies of human disease states. There are significant technical issues specific to utilizing clinical tissue samples which have yet to be rigorously addressed and completely overcome. Precise, quantitative measurement of gene expression profiles from specific cell populations is at hand, offering the scientific community the first comprehensive view of the in vivo molecular anatomy of normal cells and their diseased counterparts. Here, we propose a model for integrating-in three dimensions-expression data obtained using the **microarray**.
CT Check Tags: Human; Male
Databases, Factual
***Gene Expression**
Genome, Human
***Oligonucleotide Array Sequence Analysis: MT, methods**
Prostate: AH, anatomy & histology
Prostate: CH, chemistry
Prostate: PA, pathology
*Prostatic Neoplasms: GE, genetics
*Prostatic Neoplasms: PA, pathology
RNA, Messenger: AN, analysis
RNA, Messenger: GE, genetics
RNA, Neoplasm: AN, analysis
RNA, Neoplasm: GE, genetics
Specimen Handling
CN 0 (RNA, Messenger); 0 (RNA, Neoplasm)

L85 ANSWER 19 OF 37 MEDLINE
AN 1999112704 MEDLINE
DN 99112704
TI Exploring the new world of the genome with DNA **microarrays**.
AU Brown P O; Botstein D
CS Department of Biochemistry, Howard Hughes Medical Institute, Stanford University School of Medicine, California 94305, USA..
pbrown@cmgm.stanford.edu
SO NATURE GENETICS, (1999 Jan) 21 (1 Suppl) 33-7. Ref: 27
Journal code: BRO. ISSN: 1061-4036.
CY United States

DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199903
EW 19990305
AB Thousands of genes are being discovered for the first time by **sequencing** the genomes of model organisms, an exhilarating reminder that much of the natural world remains to be explored at the molecular level. DNA **microarrays** provide a natural vehicle for this exploration. The model organisms are the first for which comprehensive genome-wide surveys of gene expression patterns or function are possible. The results can be viewed as maps that reflect the order and logic of the genetic program, rather than the physical order of genes on chromosomes. Exploration of the genome using DNA **microarrays** and other genome-scale technologies should narrow the gap in our knowledge of gene function and molecular biology between the currently-favoured model organisms and other species.
CT Check Tags: Animal; Human
Chromosome Mapping
Databases, Factual
*DNA Probes
Gene Expression
***Genome**
*Molecular Probe Techniques
Molecular Probe Techniques: EC, economics
Oligonucleotide Array Sequence Analysis: EC, economics
***Oligonucleotide Array Sequence Analysis: MT, methods**
Sequence Analysis, DNA
CN 0 (DNA Probes)

L85 ANSWER 20 OF 37 MEDLINE
AN 1999112703 MEDLINE
DN 99112703
TI Options available--from start to finish--for obtaining expression data by **microarray** [published erratum appears in Nat Genet 1999 Feb;21(2):241].
AU Bowtell D D
CS Peter MacCallum Cancer Institute, Melbourne, Victoria, Australia.. d.bowtell@pmci.unimelb.edu.au
SO NATURE GENETICS, (1999 Jan) 21 (1 Suppl) 25-32. Ref: 35
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199903
AB The excitement surrounding **microarray** technology has been tempered by the limited ability of the general biomedical research community to gain access to it. Given the hardware required for exploitation of the technology is becoming increasingly available, it is an appropriate moment to review options, be they commercially or publically available. Here, we provide a snapshot of the rapidly changing field of **microarray**-based RNA expression analysis and consider the components and procedures for putting together a complete system.
CT Check Tags: Animal; Human
Bioethics
Cell Line
Cloning, Molecular
Database Management Systems
Expressed Sequence Tags
***Gene Expression**
Genome

***Oligonucleotide Array Sequence Analysis: EC, economics**
***Oligonucleotide Array Sequence Analysis: IS, instrumentation**
Oligonucleotide Array Sequence Analysis: MT, methods
Saccharomyces cerevisiae
Tissue Banks

L85 ANSWER 21 OF 37 MEDLINE
AN 1999112702 MEDLINE
DN 99112702
TI High density synthetic oligonucleotide arrays.
AU Lipshutz R J; Fodor S P; **Gingeras T R**; Lockhart D J
CS Affymetrix, Inc., Santa Clara, California 95051, USA.. rob_lipshutz@affymetrix.com
SO NATURE GENETICS, (1999 Jan) 21 (1 Suppl) 20-4. Ref: 32
Journal code: BRO. ISSN: 1061-4036.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
General Review; (REVIEW)
(REVIEW, TUTORIAL)
LA English
FS Priority Journals
EM 199903
EW 19990305
AB Experimental genomics involves taking advantage of sequence information to investigate and understand the workings of genes, cells and organisms. We have developed an approach in which sequence information is used directly to design high-density, two-dimensional rays of synthetic oligonucleotides. The GeneChipe probe arrays are made using spatially patterned, light-directed combinatorial chemical synthesis and contain up to hundreds of thousands of different oligonucleotides on a small glass surface. The arrays have been designed and used for quantitative and highly parallel measurements of gene expression, to discover polymorphic loci and to detect the presence of thousands of alternative alleles. Here, we describe the fabrication of the arrays, their design and some specific applications to high-throughput genetic and cellular analysis.
CT Check Tags: Animal; Human
Base Sequence
Database Management Systems
*Gene Expression
*Genotype
***Oligonucleotide Array Sequence Analysis: MT, methods**
*Oligonucleotides: CS, chemical synthesis
CN 0 (Oligonucleotides)

L85 ANSWER 22 OF 37 MEDLINE
AN 1999102443 MEDLINE
DN 99102443
TI Mycobacterium species identification and rifampin resistance testing with high-density DNA probe arrays.
AU Troesch A; Nguyen H; Miyada C G; Desvarenne S; **Gingeras T R**; Kaplan P M; Cros P; Mabilat C
CS bioMerieux, 69280 Marcy-L'Etoile, France.. alain_troesch@affymetrix.com
SO JOURNAL OF CLINICAL MICROBIOLOGY, (1999 Jan) 37 (1) 49-55.
Journal code: HSH. ISSN: 0095-1137.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199904
EW 19990402
AB Species identification within the genus Mycobacterium and subsequent antibiotic susceptibility testing still rely on time-consuming, culture-based methods. Despite the recent development of DNA probes, which greatly reduce assay time, there is a need for a single platform assay capable of answering the multitude of diagnostic questions associated with this genus. We describe the use of a DNA probe array based on two sequence

databases: one for the species identification of mycobacteria (82 unique 16S rRNA sequences corresponding to 54 phenotypical species) and the other for detecting Mycobacterium tuberculosis rifampin resistance (rpoB alleles). Species identification or rifampin resistance was determined by hybridizing fluorescently labeled, amplified genetic material generated from bacterial colonies to the array. Seventy mycobacterial isolates from 27 different species and 15 rifampin-resistant M. tuberculosis strains were tested. A total of 26 of 27 species were correctly identified as well as all of the rpoB mutants. This parallel testing format opens new perspectives in terms of patient management for bacterial diseases by allowing a number of genetic tests to be simultaneously run.

CT Check Tags: Human
*Antibiotics, Antitubercular: PD, pharmacology
Drug Resistance, Microbial: GE, genetics
DNA Mutational Analysis
*DNA Probes
DNA, Bacterial: GE, genetics
*Microbial Sensitivity Tests: MT, methods
*Mycobacterium: CL, classification
*Mycobacterium: DE, drug effects
Mycobacterium tuberculosis: DE, drug effects
Mycobacterium tuberculosis: GE, genetics
Mycobacterium tuberculosis: IP, isolation & purification
Nucleic Acid Hybridization: MT, methods
*Rifampin: PD, pharmacology
RNA, Ribosomal, 16S: GE, genetics
Species Specificity
RN 13292-46-1 (Rifampin)
CN 0 (Antibiotics, Antitubercular); 0 (DNA Probes); 0 (DNA, Bacterial); 0 (RNA, Ribosomal, 16S)

L85 ANSWER 23 OF 37 MEDLINE
AN 1998334290 MEDLINE
DN 98334290
TI Comparative performance of high-density oligonucleotide sequencing and dideoxynucleotide sequencing of HIV type 1 pol from clinical samples.
AU Gunthard H F; Wong J K; Ignacio C C; Havlir D V; Richman D D
CS Department of Pathology, School of Medicine, University of California at San Diego, La Jolla 92093-0679, USA.
NC K 11 AI01361 (NIAID)
AI 27670 (NIAID)
AI 38858 (NIAID)
+
SO AIDS RESEARCH AND HUMAN RETROVIRUSES, (1998 Jul 1) 14 (10) 869-76.
Journal code: ART. ISSN: 0889-2229.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199811
EW 19981103
AB The performance of the high-density oligonucleotide array methodology (**GeneChip**) in detecting drug resistance mutations in HIV-1 pol was compared with that of automated dideoxynucleotide sequencing (ABI) of clinical samples, viral stocks, and plasmid-derived NL4-3 clones. Sequences from 29 clinical samples (plasma RNA, n = 17; lymph node RNA, n = 5; lymph node DNA, n = 7) from 12 patients, from 6 viral stock RNA samples, and from 13 NL4-3 clones were generated by both methods. Editing was done independently by a different investigator for each method before comparing the sequences. In addition, NL4-3 wild type (WT) and mutants were mixed in varying concentrations and sequenced by both methods. Overall, a concordance of 99.1% was found for a total of 30,865 bases compared. The comparison of clinical samples (plasma RNA and lymph node RNA and DNA) showed a slightly lower match of base calls, 98.8% for 19,831 nucleotides compared (protease region, 99.5%, n = 8272; RT region, 98.3%, n = 11,316), than for viral stocks and NL4-3 clones (protease region,

99.8%; RT region, 99.5%). Artificial mixing experiments showed a bias toward calling wild-type bases by **GeneChip**. Discordant base calls are most likely due to differential detection of mixtures. The concordance between **GeneChip** and ABI was high and appeared dependent on the nature of the templates (directly amplified versus cloned) and the complexity of mixes.

CT Check Tags: Comparative Study; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Anti-HIV Agents: PD, pharmacology
Drug Resistance, Microbial
*HIV Infections: VI, virology
*HIV Protease: GE, genetics
HIV Protease Inhibitors: PD, pharmacology
HIV-1: DE, drug effects
*HIV-1: EN, enzymology
HIV-1: GE, genetics
*HIV-1 Reverse Transcriptase: GE, genetics
Indinavir: PD, pharmacology
Oligonucleotides
Polymerase Chain Reaction
Reverse Transcriptase Inhibitors: PD, pharmacology
RNA, Viral: BL, blood
Sensitivity and Specificity
***Sequence Analysis, DNA: MT, methods**
Zidovudine: PD, pharmacology

RN 150378-17-9 (Indinavir); 30516-87-1 (Zidovudine)

CN EC 2.7.7.- (HIV-1 Reverse Transcriptase); EC 3.4.23.- (HIV Protease); 0 (Anti-HIV Agents); 0 (HIV Protease Inhibitors); 0 (Oligonucleotides); 0 (Reverse Transcriptase Inhibitors); 0 (RNA, Viral)

L85 ANSWER 24 OF 37 MEDLINE

AN 1998248685 MEDLINE

DN 98248685

TI Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic Mycobacterium DNA arrays.

AU **Gingeras T R**; Ghandour G; Wang E; Berno A; Small P M; Drobniewski F; Alland D; Desmond E; Holodniy M; Drenkow J

CS Affymetrix, Santa Clara, California 95051, USA..
tom_gingeras@affymetrix.com

NC 1R43A140400

SO GENOME RESEARCH, (1998 May) 8 (5) 435-48.
Journal code: CES. ISSN: 1088-9051.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals

OS GENBANK-AF059766; GENBANK-AF059767; GENBANK-AF059768; GENBANK-AF059769; GENBANK-AF059770; GENBANK-AF059771; GENBANK-AF059772; GENBANK-AF059773; GENBANK-AF059774; GENBANK-AF059775; GENBANK-AF059776; GENBANK-AF059777; GENBANK-AF059778; GENBANK-AF059779; GENBANK-AF059780; GENBANK-AF059781; GENBANK-AF059782; GENBANK-AF059783; GENBANK-AF059784; GENBANK-AF059785; GENBANK-AF059786; GENBANK-AF059787; GENBANK-AF059788; GENBANK-AF059789; GENBANK-AF059790; GENBANK-AF059791; GENBANK-AF059792; GENBANK-AF059793; GENBANK-AF059794; GENBANK-AF059795

EM 199810

AB High-density oligonucleotide arrays can be used to rapidly examine large amounts of DNA sequence in a high throughput manner. An array designed to determine the specific nucleotide sequence of 705 bp of the rpoB gene of Mycobacterium tuberculosis accurately detected rifampin resistance associated with mutations of 44 clinical isolates of M. tuberculosis. The nucleotide sequence diversity in 121 Mycobacterial isolates (comprised of 10 species) was examined by both conventional dideoxynucleotide sequencing of the rpoB and 16S genes and by analysis of the rpoB oligonucleotide array hybridization patterns. Species identification for each of the isolates was similar irrespective of whether 16S sequence, rpoB sequence, or the pattern of rpoB hybridization was used. However, for several

species, the number of alleles in the 16S and rpoB gene sequences provided discordant estimates of the genetic diversity within a species. In addition to confirming the array's intended utility for sequencing the region of M. tuberculosis that confers rifampin resistance, this work demonstrates that this array can identify the species of nontuberculous Mycobacteria. This demonstrates the general point that DNA microarrays that sequence important genomic regions (such as drug resistance or pathogenicity islands) can simultaneously identify species and provide some insight into the organism's population structure.

CT Check Tags: Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Alleles
Drug Resistance, Microbial: GE, genetics
DNA-Directed RNA Polymerase: GE, genetics
*DNA, Bacterial: AN, analysis
Gene Frequency
Genes, Structural, Bacterial
Genotype
Molecular Sequence Data
Mutagenesis
Mycobacterium: DE, drug effects
*Mycobacterium: GE, genetics
*Mycobacterium: IP, isolation & purification
Mycobacterium tuberculosis: DE, drug effects
Mycobacterium tuberculosis: GE, genetics
Nucleic Acid Hybridization: MT, methods
Oligonucleotides: AN, analysis
Polymorphism (Genetics)
Rifampin: PD, pharmacology
RNA, Ribosomal, 16S: GE, genetics
Sequence Analysis, DNA
Species Specificity

RN 13292-46-1 (Rifampin)

CN EC 2.7.7.6 (DNA-Directed RNA Polymerase); 0 (DNA, Bacterial); 0 (Oligonucleotides); 0 (RNA polymerase beta subunit); 0 (RNA, Ribosomal, 16S)

L85 ANSWER 25 OF 37 MEDLINE

AN 1998248615 MEDLINE

DN 98248615

TI Large-scale identification, mapping, and genotyping of single-nucleotide polymorphisms in the human genome.

AU Wang D G; Fan J B; Siao C J; Berno A; Young P; Sapolsky R; Ghandour G; Perkins N; Winchester E; Spencer J; Kruglyak L; Stein L; Hsie L; Topaloglou T; Hubbell E; Robinson E; Mittmann M; Morris M S; Shen N; Kilburn D; Rioux J; Nusbaum C; Rozen S; Hudson T J; Lander E S; et al

CS Whitehead Institute for Biomedical Research, Nine Cambridge Center, Cambridge, MA 02142, USA.

NC HG00098 (NHGRI)
HG01323 (NHGRI)

SO SCIENCE, (1998 May 15) 280 (5366) 1077-82.
Journal code: UJ7. ISSN: 0036-8075.

CY United States

DT Journal; Article; (JOURNAL ARTICLE)

LA English

FS Priority Journals; Cancer Journals

OS GENBANK-G42906; GENBANK-G42907; GENBANK-G42908; GENBANK-G42909; GENBANK-G42910; GENBANK-G42911; GENBANK-G42912; GENBANK-G42913; GENBANK-G42914; GENBANK-G42915; GENBANK-G42916; GENBANK-G42917; GENBANK-G42918; GENBANK-G42919; GENBANK-G42920; GENBANK-G42921; GENBANK-G42922; GENBANK-G42923; GENBANK-G42924; GENBANK-G42925; GENBANK-G42926; GENBANK-G42927; GENBANK-G42928; GENBANK-G42929; GENBANK-G42930; GENBANK-G42931; GENBANK-G42932; GENBANK-G42933; GENBANK-G42934; GENBANK-G42935

EM 199808

AB Single-nucleotide polymorphisms (SNPs) are the most frequent type of variation in the human genome, and they provide powerful tools for a

variety of medical genetic studies. In a large-scale survey for SNPs, 2.3 megabases of human genomic DNA was examined by a combination of gel-based **sequencing** and high-density variation-detection DNA chips. A total of 3241 candidate SNPs were identified. A genetic map was constructed showing the location of 2227 of these SNPs. Prototype genotyping chips were developed that allow simultaneous genotyping of 500 SNPs. The results provide a characterization of human diversity at the nucleotide level and demonstrate the feasibility of large-scale identification of human SNPs.

CT Check Tags: Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.

Algorithms
Alleles
*Chromosome Mapping: MT, methods
Databases, Factual
*Deoxyribonucleotides: GE, genetics
Dinucleoside Phosphates
DNA, Complementary
Gene Expression
Genetic Markers
*Genetic Techniques
***Genome, Human**
*Genotype
Heterozygote
Homozygote
Nucleic Acid Hybridization
Polymerase Chain Reaction
*Polymorphism (Genetics)
Reproducibility of Results
Sequence Analysis, DNA
Sequence Tagged Sites
Variation (Genetics)

RN 2382-65-2 (cytidylyl-3'-5'-guanosine)
CN 0 (Deoxyribonucleotides); 0 (Dinucleoside Phosphates); 0 (DNA, Complementary); 0 (Genetic Markers)

L85 ANSWER 26 OF 37 MEDLINE
AN 1998030190 MEDLINE
DN 98030190
TI Contribution of novel choline-binding proteins to adherence, colonization and immunogenicity of Streptococcus pneumoniae.
AU **Rosenow C**; Ryan P; Weiser J N; Johnson S; Fontan P; Ortqvist A; Masure H R
CS The Laboratory of Molecular Infectious Diseases, The Rockefeller University, New York, NY 10021-6399, USA.
NC AI 36445 (NIAID)
AI38446 (NIAID)
SO MOLECULAR MICROBIOLOGY, (1997 Sep) 25 (5) 819-29.
Journal code: MOM. ISSN: 0950-382X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199803
EW 19980305
AB The surface of Streptococcus pneumoniae is decorated with a family of choline-binding proteins (CBPs) that are non-covalently bound to the phosphorylcholine of the teichoic acid. Two examples (PspA, a protective antigen, and LytA, the major autolysin) have been well characterized. We identified additional CPBs and characterized a new CBP, CbpA, as an adhesin and a determinant of virulence. Using choline immobilized on a solid matrix, a mixture of proteins from a pspA-deficient strain of pneumococcus was eluted in a choline-dependent fashion. Antisera to these proteins passively protected mice challenged in the peritoneum with a lethal dose of pneumococci. The predominant component of this mixture, CbpA, is a 75-kDa surface-exposed protein that reacts with human convalescent antisera. The deduced sequence from the corresponding gene

showed a chimeric architecture with a unique N-terminal region and a C-terminal domain consisting of 10 repeated choline-binding domains nearly identical to PspA. A cbpA-deficient mutant showed a >50% reduction in adherence to cytokine-activated human cells and failed to bind to immobilized sialic acid or lacto-N-neotetraose, known pneumococcal ligands on eukaryotic cells. Carriage of this mutant in an animal model of nasopharyngeal colonization was reduced 100-fold. There was no difference between the parent strain and this mutant in an intraperitoneal model of sepsis. These data for CbpA extend the important functions of the CBP family to bacterial adherence and identify a pneumococcal vaccine candidate.

CT Check Tags: Animal; Human; Support, Non-U.S. Gov't; Support, U.S. Gov't, P.H.S.
Amino Acid Sequence
*Bacterial Adhesion: PH, physiology
Bacterial Proteins: AN, analysis
Bacterial Proteins: GE, genetics
Carrier Proteins: AN, analysis
Carrier Proteins: GE, genetics
*Carrier Proteins: PH, physiology
Cell Line: MI, microbiology
*Choline: ME, metabolism
Cloning, Molecular
Gene Expression
Mice
Molecular Sequence Data
Mutation
Phenotype
Rats
Rats, Sprague-Dawley
Sequence Analysis, DNA
Streptococcus pneumoniae: CH, chemistry
*Streptococcus pneumoniae: GD, growth & development
*Streptococcus pneumoniae: IM, immunology
Variation (Genetics)

RN 62-49-7 (Choline)
CN 0 (Bacterial Proteins); 0 (Carrier Proteins)

L85 ANSWER 27 OF 37 MEDLINE
AN 97008550 MEDLINE
DN 97008550
TI The C. elegans expression pattern database: a beginning.
AU Hope I A; Albertson D G; Martinelli S D; Lynch A S; Sonnhammer E; Durbin R
CS Department of Biology, University of Leeds, UK.. i.a.hope@leeds.ac.uk
SO TRENDS IN GENETICS, (1996 Sep) 12 (9) 370-1.
Journal code: WEK. ISSN: 0168-9525.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
EM 199702
CT Check Tags: Animal; Male
Caenorhabditis elegans: EM, embryology
Caenorhabditis elegans: GD, growth & development
*Caenorhabditis elegans: GE, genetics
***Databases, Factual**
Gene Expression Regulation
Genes, Reporter
Genome
In Situ Hybridization
Lac Operon: GE, genetics
Luminescent Proteins: GE, genetics
Recombinant Fusion Proteins: BI, biosynthesis
Recombinant Fusion Proteins: GE, genetics
Transcription, Genetic
RN 147336-22-9 (green fluorescent protein)
CN 0 (Luminescent Proteins); 0 (Recombinant Fusion Proteins)

L85 ANSWER 28 OF 37 MEDLINE
AN 97002455 MEDLINE
DN 97002455
TI Accessing genetic information with high-density DNA **arrays**.
AU Chee M; Yang R; Hubbell E; Berno A; Huang X C; Stern D; Winkler J; Lockhart D J; Morris M S; Fodor S P
CS Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA.
NC 5RO1HG00813 (NHGRI)
SO SCIENCE, (1996 Oct 25) 274 (5287) 610-4.
Journal code: UJ7. ISSN: 0036-8075.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 199701
AB Rapid access to genetic information is central to the revolution taking place in molecular genetics. The simultaneous analysis of the entire human mitochondrial genome is described here. DNA **arrays** containing up to 135,000 probes complementary to the 16.6-kilobase human mitochondrial genome were generated by light-directed chemical synthesis. A two-color labeling scheme was developed that allows simultaneous comparison of a polymorphic target to a reference DNA or RNA. Complete hybridization patterns were revealed in a matter of minutes. **Sequence** polymorphisms were detected with single-base resolution and unprecedented efficiency. The methods described are generic and can be used to address a variety of questions in molecular genetics including gene expression, genetic linkage, and genetic variability.
CT Check Tags: Human; Support, U.S. Gov't, P.H.S.
Algorithms
Base Composition
Base Sequence
Cloning, Molecular
*DNA, Mitochondrial: GE, genetics
Fluoresceins
Gene Expression
***Genome**
*Mitochondria: GE, genetics
***Nucleic Acid Hybridization**
*Oligonucleotide Probes
Phycoerythrin
Polymerase Chain Reaction
Polymorphism (Genetics)
Sequence Analysis, DNA
Variation (Genetics)
RN 11016-17-4 (Phycoerythrin); 2321-07-5 (Fluorescein)
CN 0 (DNA, Mitochondrial); 0 (Fluoresceins); 0 (Oligonucleotide Probes)

L85 ANSWER 29 OF 37 MEDLINE
AN 96417859 MEDLINE
DN 96417859
TI Pyruvate oxidase, as a determinant of virulence in Streptococcus pneumoniae.
AU Spellerberg B; Cundell D R; Sandros J; Pearce B J; Idanpaan-Heikkila I; **Rosenow C**; Masure H R
CS Laboratory of Molecular Infectious Diseases, The Rockefeller University, New York 10021-6399, USA.
SO MOLECULAR MICROBIOLOGY, (1996 Feb) 19 (4) 803-13.
Journal code: MOM. ISSN: 0950-382X.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-L39074
EM 199702
AB Pneumococcus has been shown to bind to epithelial cells of the nasopharynx

and lung, and to endothelial cells of the peripheral vasculature. To characterize bacterial elements required for attachment to these cell types, a library of genetically altered pneumococci with defects in exported proteins was screened for the loss of attachment to glycoconjugates representative of the nasopharyngeal cell receptor, type II lung cells (LC) and human endothelial cells (EC). A mutant was identified which showed a greater than 70% loss in the ability to attach to all cell types. This mutant also showed decreased adherence to the glycoconjugates containing the terminal sugar residues GalNAcbeta1-3Gal, GalNAcbeta1-4Gal and the carbohydrate GlcNAc, which are proposed components of the pneumococcal receptors specific to the surfaces of LC and EC. Analysis of the locus altered in this mutant revealed a gene, spxB, that encodes a member of the family of bacterial pyruvate oxidases which decarboxylates pyruvate to acetyl phosphate plus H2O2 and CO2. This mutant produced decreased concentrations of H2O2 and failed to grow aerobically in a chemically defined medium, unless supplemented with acetate which presumably restores acetyl phosphate levels by the action of acetate kinase, further suggesting that spxB encodes a pyruvate oxidase. The addition of acetate to the growth medium restored the adherence properties of the mutant indicating a link between the enzyme and the expression of bacterial adhesins. A defect in spxB corresponded to impaired virulence of the mutant in vivo. Compared to the parent strain, an spxB mutant showed reduced virulence in animal models for nasopharyngeal colonization, pneumonia, and sepsis. We propose that a mutation in spxB leads to down-regulation of the multiple adhesive properties of pneumococcus which, in turn, may correlate to diminished virulence in vivo.

CT Check Tags: Animal; Human; Support, Non-U.S. Gov't
*Bacterial Adhesion
Bacterial Proteins: SE, secretion
Base Sequence
Carbohydrate Sequence
Cells, Cultured
Eukaryotic Cells: MI, microbiology
Glycoconjugates: ME, metabolism
Hydrogen Peroxide: ME, metabolism
Lung: CY, cytology
Lung: MI, microbiology
Molecular Sequence Data
Mutagenesis
Nasopharynx: CY, cytology
Nasopharynx: MI, microbiology
*Pyruvate Oxidase
Rabbits
Sequence Analysis, DNA
Streptococcus pneumoniae: EN, enzymology
Streptococcus pneumoniae: GE, genetics
*Streptococcus pneumoniae: PY, pathogenicity
Virulence: GE, genetics

RN 7722-84-1 (Hydrogen Peroxide)
CN EC 1.2.3.3 (Pyruvate Oxidase); 0 (Bacterial Proteins); 0 (Glycoconjugates)

L85 ANSWER 30 OF 37 MEDLINE
AN 95277534 MEDLINE
DN 95277534
TI [IMAGE: molecular integration of the analysis of the human genome and its expression].
IMAGE: integration au niveau moleculaire de l'analyse du genome humain et de son expression.
AU Auffray C; Behar G; Bois F; Bouchier C; Da Silva C; Devignes M D; Duprat S; Houlgatte R; Jumeau M N; Lamy B; et al
CS Genexpress, Genethon, Evry, France.
SO COMPTES RENDUS DE L ACADEMIE DES SCIENCES. SERIE III, SCIENCES DE LA VIE, (1995 Feb) 318 (2) 263-72.
Journal code: CA1. ISSN: 0764-4469.
CY France

DT Journal; Article; (JOURNAL ARTICLE)
LA French
FS Priority Journals
OS GENBANK-F00001; GENBANK-F00002; GENBANK-F00003; GENBANK-F00004; GENBANK-F00005; GENBANK-F00006; GENBANK-F00007; GENBANK-F00008; GENBANK-F00009; GENBANK-F00010; GENBANK-F00011; GENBANK-F00012; GENBANK-F00013; GENBANK-F00014; GENBANK-F00015; GENBANK-F00016; GENBANK-F00017; GENBANK-F00018; GENBANK-F00019; GENBANK-F00020; GENBANK-F00021; GENBANK-F00022; GENBANK-F00023; GENBANK-F00024; GENBANK-F00025; GENBANK-F00026; GENBANK-F00027; GENBANK-F00028; GENBANK-F00029; GENBANK-F00030
EM 199509
AB We have developed an integrated approach for the analysis of human cDNA libraries from neuromuscular tissues, based on the acquisition of primary structural, expression and mapping data. 26,938 **sequence** signatures (over 7 million bases) have been derived from both ends of skeletal muscle and brain cDNA clones. Primary redundancy analysis and classification of database similarities made it possible to characterize by structural data about 8,000 human gene transcripts, the majority of which is catalogued for the first time. Collecting hybridization signatures of complex cDNA probes derived from the tissues of origin to cDNA clones **arrayed** on high density filters provided a global and quantifiable view of the complexity and level of expression of the different transcripts. The development of 2,792 eSTS markers amplifiable by PCR defined the chromosomal localization of some 2,500 genes corresponding to the transcripts **sequenced**. The data collected are part of the corpus of the human gene transcript catalog and the genic map of the human genome.
CT Check Tags: Human; Support, Non-U.S. Gov't
Brain Chemistry
English Abstract
Gene Expression
***Genome, Human**
***Genomic Library**
***Information Systems**
Molecular Sequence Data
Muscles: CH, chemistry
Nucleic Acid Hybridization
Sequence Analysis, DNA

L85 ANSWER 31 OF 37 MEDLINE
AN 95173087 MEDLINE
DN 95173087
TI Characterization and localization of the KpsE protein of Escherichia coli K5, which is involved in polysaccharide export.
AU **Rosenow C**; Esumeh F; Roberts I S; Jann K
CS Max-Planck-Institut fur Immunobiologie, Freiburg, Germany..
SO JOURNAL OF BACTERIOLOGY, (1995 Mar) 177 (5) 1137-43.
Journal code: HH3. ISSN: 0021-9193.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 199506
AB In Escherichia coli with group II capsules, the synthesis and cellular expression of capsular polysaccharide are encoded by the kps gene cluster. This gene cluster is composed of three regions. The central region 2 encodes proteins involved in polysaccharide synthesis, and the flanking regions 1 and 3 direct the translocation of the finished polysaccharide across the cytoplasmic membrane and its surface expression. The kps genes of the K5 polysaccharide, which is a group II capsular polysaccharide, have been cloned and sequenced. Region 1 contains the kpsE, -D, -U, -C, and -S genes. In this communication we describe the KpsE protein, the product of the kpsE gene. A truncated kpsE gene was fused with a truncated beta-galactosidase gene to generate a fusion protein containing the first 375 amino acids of beta-galactosidase and amino acids 67 to 382 of KpsE

(KpsE'). This fusion protein was isolated and cleaved with factor Xa, and the purified KpsE' was used to immunize rabbits. Intact KpsE was extracted from the membranes of a KpsE-overexpressing recombinant strain with octyl-beta-glucoside. It was purified by affinity chromatography with immobilized anti-KpsE antibodies. Cytofluorometric analysis using the anti-KpsE antibodies with whole cells and spheroplasts, as well as sodium dodecyl sulfate-polyacrylamide gel electrophoresis and Western blotting (immunoblotting) of proteins from spheroplasts and membranes before and after treatment with proteinase K, indicated that the KpsE protein is associated with the cytoplasmic membrane and has an exposed periplasmic domain.(ABSTRACT TRUNCATED AT 250 WORDS)

CT Check Tags: Support, Non-U.S. Gov't
Amino Acid Sequence
Bacterial Capsules: ME, metabolism
Bacterial Proteins: GE, genetics
Bacterial Proteins: IM, immunology
*Bacterial Proteins: IP, isolation & purification
Blotting, Western
*Cell Membrane: CH, chemistry
*Escherichia coli: CH, chemistry
Escherichia coli: GE, genetics
Membrane Proteins: GE, genetics
Membrane Proteins: IM, immunology
*Membrane Proteins: IP, isolation & purification
Molecular Sequence Data
Mutagenesis, Insertional
Polysaccharides, Bacterial: ME, metabolism
Recombinant Fusion Proteins: BI, biosynthesis
Recombinant Fusion Proteins: IM, immunology
Sequence Analysis
Subcellular Fractions: CH, chemistry
Subcellular Fractions: IM, immunology

CN 0 (kpsE protein); 0 (Bacterial Capsules); 0 (Bacterial Proteins); 0 (Membrane Proteins); 0 (Polysaccharides, Bacterial); 0 (Recombinant Fusion Proteins)

GEN kpsE

L85 ANSWER 32 OF 37 MEDLINE
AN 93081916 MEDLINE
DN 93081916
TI Hybridization fingerprinting of high-density cDNA-library **arrays** with cDNA pools derived from whole tissues.
AU Gress T M; Hoheisel J D; Lennon G G; Zehetner G; Lehrach H
CS Imperial Cancer Research Fund, London, UK..
SO MAMMALIAN GENOME, (1992) 3 (11) 609-19.
Journal code: BES. ISSN: 0938-8990.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
OS GENBANK-X65374; GENBANK-X65375; GENBANK-X65376; GENBANK-X65377; GENBANK-X65378; GENBANK-X65379; GENBANK-X65380; GENBANK-X65381; GENBANK-X65382; GENBANK-X65383; GENBANK-X65384; GENBANK-X65385; GENBANK-X65386; GENBANK-X65387; GENBANK-X65388; GENBANK-X65389; GENBANK-X65390; GENBANK-X65391; GENBANK-X65392; GENBANK-X65393; GENBANK-X65268; GENBANK-X65269; GENBANK-X65270; GENBANK-X65271; GENBANK-X65272; GENBANK-X65273; GENBANK-X65274; GENBANK-X65275
EM 199303
AB As part of an integrated mapping and **sequencing** analysis of genomes, we have developed an approach allowing the characterization of large numbers of cDNA library clones with a minimal number of experiments. Three basic elements used in the analysis of cDNA libraries are responsible for the high efficiency of this new approach: (1) high-density library **arrays** allowing thousands of clones to be screened simultaneously; (2) hybridization fingerprinting techniques to identify clones abundantly expressed in specific tissues (by hybridizations with

labeled tissue cDNA pools) and to avoid the repeated selection of identical clones and of clones containing noncoding inserts; and (3) a computerized system for the evaluation of hybridization data. To demonstrate the feasibility of this approach, we hybridized high-density cDNA library **arrays** of human fetal brain and embryonal Drosophila with radiolabeled cDNA pools derived from whole mouse tissues. Fingerprints of the library **arrays** were generated, localizing clones containing cDNA **sequences** from mRNAs expressed at middle to high abundance (> 0.1-0.15%) in the respective tissue. Partial **sequencing** data from a number of clones abundantly expressed in several tissues were generated to demonstrate the value of the approach, especially for the selection of cDNA clones for the analyses of genomes based on expressed **sequence** tagged sites. Data obtained by the technique described will ultimately be correlated with additional transcriptional and **sequence** information for the same library clones and with genomic mapping information in a relational database.

CT Check Tags: Animal; Human; Support, Non-U.S. Gov't
Base Sequence
Blotting, Northern
Drosophila: EM, embryology
Drosophila: GE, genetics
*DNA: GE, genetics
*DNA Fingerprinting
Genomic Library
Image Processing, Computer-Assisted
Molecular Sequence Data
Nucleic Acid Hybridization
Polymerase Chain Reaction
Sequence Analysis
***Transcription, Genetic**
RN 9007-49-2 (DNA)

L85 ANSWER 33 OF 37 MEDLINE
AN 89145205 MEDLINE
DN **89145205**
TI Transcription-based amplification system and detection of amplified human immunodeficiency virus type 1 with a bead-based sandwich hybridization format.
AU Kwoh D Y; Davis G R; Whitfield K M; Chappelle H L; DiMichele L J; Gingeras T R
CS SISKA Diagnostics, San Diego, CA 92138-9216.
NC NO1-HB-6-7019 (NHLBI)
SO PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1989 Feb) 86 (4) 1173-7.
Journal code: PV3. ISSN: 0027-8424.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals; Cancer Journals
EM 198906
AB The in vitro amplification of biologically important nucleic acids has proceeded principally by a strategy of DNA replication. Polymerase chain reaction was the first such protocol to achieve this goal. In this report, a transcription-based amplification system (TAS) is described. Each cycle of the TAS is composed of two steps. The first is a cDNA synthesis step that produces one copy of a double-stranded DNA template for each copy of RNA or DNA target nucleic acid. During the course of this cDNA synthesis step, a sequence recognized by a DNA-dependent RNA polymerase is inserted into the cDNA copy of the target sequence to be amplified. The second step is the amplification of the target sequence by the transcription of the cDNA template into multiple copies of RNA. This procedure has been applied to the detection of human immunodeficiency virus type 1 (HIV-1)-infected cells. After four cycles of TAS, the amplification of the vif region of the HIV-1 RNA genome was measured to be, on the average, 38- to 47-fold per cycle, resulting in a 2-5 x 10(6)-fold increase in the copy number of the original target sequence. This amplification by the TAS protocol

allows the detection of fewer than one HIV-1-infected CEM cell in a population of 10(6) uninfected CEM cells. Detection of the TAS-generated RNA from HIV-1-infected cells can easily be accomplished by means of a bead-based sandwich hybridization protocol, which provides additional specificity for the identification of the amplified HIV-1-specific sequence.

CT Check Tags: Human; Support, U.S. Gov't, P.H.S.
Cell Line
Cell Transformation, Viral
*Gene Amplification
*Genes, Viral
*HIV-1: GE, genetics
Nucleic Acid Hybridization
Oligonucleotide Probes
RNA, Viral: GE, genetics
RNA, Viral: IP, isolation & purification
*Transcription, Genetic

CN 0 (Oligonucleotide Probes); 0 (RNA, Viral)

L85 ANSWER 34 OF 37 MEDLINE
AN 82150167 MEDLINE
DN **82150167**
TI A semi-automated method for the reading of nucleic acid sequencing gels.
AU Gingeras T R; Rice P; Roberts R J
NC CA 27275 (NCI)
SO NUCLEIC ACIDS RESEARCH, (1982 Jan 11) 10 (1) 103-14.
Journal code: O8L. ISSN: 0301-5610.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198207
AB A collection of computer programs is described which permit automatic entering of nucleotide sequence data directly from an autoradiograph into a computer. This collection, called DIGITPAD, makes use of a digitizing tablet for the data entry and allows the rapid and accurate transfer of the sequence into the computer.
CT Check Tags: Support, U.S. Gov't, P.H.S.
*Base Sequence
*Computers
*DNA
Methods
RN 9007-49-2 (DNA)

L85 ANSWER 35 OF 37 MEDLINE
AN 81015439 MEDLINE
DN **81015439**
TI Steps toward computer analysis of nucleotide sequences.
AU Gingeras T R; Roberts R J
NC CA 13106 (NCI)
1R01-CA27275-01 (NCI)
SO SCIENCE, (1980 Sep 19) 209 (4463) 1322-8.
Journal code: UJ7. ISSN: 0036-8075.
CY United States
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 198101
AB Advances in recombinant DNA technology have allowed the isolation of large numbers of biologically interesting fragments of DNA. Concomitant improvements in methods for nucleic acid sequencing have led many investigators to characterize their clones by sequencing them. This has resulted in the accumulation of such large amounts of sequence data that computer-assisted methods, with programs directed toward the manipulation of nucleic acid sequences, have become indispensable during the collection and analysis of that data.

CT Check Tags: Support, U.S. Gov't, P.H.S.
Autoanalysis
*Base Sequence
*Computers
DNA Restriction Enzymes
DNA, Viral
Genes, Structural
Hydrogen Bonding
Nucleic Acid Conformation
Nucleic Acid Precursors: GE, genetics
*Nucleic Acids
RNA, Transfer: GE, genetics
Substrate Specificity
RN 9014-25-9 (RNA, Transfer)
CN EC 3.1.21 (DNA Restriction Enzymes); 0 (DNA, Viral); 0 (Nucleic Acid Precursors); 0 (Nucleic Acids)

=> d l65 44 all

L65 ANSWER 44 OF 46 MEDLINE
AN 79074274 MEDLINE
DN 79074274
TI A computer assisted method for the determination of restriction enzyme recognifion sites.
AU **Gingeras T R**; MIlazzo J P; Roberts R J
SO NUCLEIC ACIDS RESEARCH, (1978 Nov) 5 (11) 4105-27.
Journal code: O8L. ISSN: 0301-5610.
CY ENGLAND: United Kingdom
DT Journal; Article; (JOURNAL ARTICLE)
LA English
FS Priority Journals
EM 197904
AB A computer program has been developed which aids in the determination of restriction enzyme recognition sequences. This is achieved by cleaving DNAs of known sequence with a restriction endonuclease and comparing the fragmentation pattern with a computer-generated set of patterns. The feasibility of this approach has been tested using fragmentation patterns of 0X174 DNA produced by enzymes of both known and unknown specificity. Recognition sequences are predicted for two restriction endonucleases (BbvI and SfaNI) using this method. In addition, recognition sequences are predicted for two other new enzymes (PvuI and MstI) using another computer-assisted method.
CT Check Tags: Support, U.S. Gov't, Non-P.H.S.; Support, U.S. Gov't, P.H.S.
Base Sequence
Computers
*DNA
*DNA Restriction Enzymes
Methods
Oligodeoxyribonucleotides: AN, analysis

=>

=> fil hcaplus

FILE 'HCAPLUS' ENTERED AT 12:51:53 ON 26 JAN 2001

held by the publishers listed in the PUBLISHER (PB) field (available for records published or updated in Chemical Abstracts after December 26, 1996), unless otherwise indicated in the original publications.

FILE COVERS 1967 - 26 Jan 2001 VOL 134 ISS 6
FILE LAST UPDATED: 25 Jan 2001 (20010125/ED)

This file contains CAS Registry Numbers for easy and accurate substance identification.

This file supports REG1stRY for direct browsing and searching of all substance data from the REGISTRY file. Enter HELP FIRST for more information.

Now you can extend your author, patent assignee, patent information, and title searches back to 1907. The records from 1907-1966 now have this searchable data in CAOLD. You now have electronic access to all of CA: 1907 to 1966 in CAOLD and 1967 to the present in HCAPLUS on STN.

=> d all tot

L108 ANSWER 1 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 2001:40773 HCAPLUS
TI **High-density microarray**-mediated gene expression profiling of Escherichia coli
AU Wei, Yan; Lee, Jian-Ming; Richmond, Craig; Blattner, Frederick R.; Rafalski, J. Antoni; LaRossa, Robert A.
CS Central Research and Development, DuPont Company, Wilmington, DE, 19880-0173, USA
SO J. Bacteriol. (2001), 183(2), 545-556
CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
CC 3 (Biochemical Genetics)
AB A nearly complete collection of 4,290 Escherichia coli open reading frames was amplified and **arrayed** in high d. on glass slides. To exploit this reagent, conditions for RNA isolation from E. coli cells, cDNA prodn. with attendant fluorescent dye incorporation, DNA-DNA **hybridization**, and **hybrid** quantitation have been established. A brief isopropyl-.beta.-D-thiogalactopyranoside (IPTG) treatment elevated lacZ, lacY, and lacA **transcript** content about 30-fold; in contrast, most other **transcript** titers remained unchanged. Distinct RNA expression patterns between E. coli cultures in the exponential and transitional phases of growth were catalogued, as were differences assocd. with culturing in minimal and rich media. The relative abundance of each **transcript** was estd. by using **hybridization** of a **genomic** DNA-derived, fluorescently labeled probe as a correction factor. This inventory provided a quant. view of the steady-state level of each mRNA species. Genes the expression of which was detected by this method were enumerated, and results were compared with the current understanding of E. coli physiol.
RE.CNT 40
RE
(1) Bachmann, B; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V2, P2460
(2) Berlyn, M; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V2, P1715
(3) Bochner, B; J Biol Chem 1982, V257, P9759 HCAPLUS
(4) Bremer, H; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V2, P1553
(5) Castanie-Cornet, M; J Bacteriol 1999, V181, P3525 HCAPLUS
(6) Chuang, S; J Bacteriol 1993, V175, P2026 HCAPLUS
(7) Cronan, J; Escherichia coli and Salmonella: cellular and molecular biology

2nd ed 1996, V1, P206
(8) DeRisi, J; Science 1997, V278, P680 HCAPLUS
(9) Green, J; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P665
(10) Greene, R; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P542
(11) Henge-Aronis, R; Bacterial stress responses 2000, P161
(12) Henge-Aronis, R; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P1497
(13) Jensen, K; J Bacteriol 1993, V175, P3401 HCAPLUS
(14) Jia, M; Physiol Genomics 2000, V3, P83
(15) Keener, J; Escherichia coli and Salmonella: cellular and molecular biology 1996, V1, P1417
(16) Kenyon, C; Proc Natl Acad Sci USA 1980, V77, P2819 HCAPLUS
(17) Kredich, N; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P514
(18) Kushner, S; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, P849
(19) LaRossa, R; Bacterial stress responses 2000, P453 HCAPLUS
(20) Landick, R; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 2000, V1, P1263
(21) Lowry, O; J Biol Chem 1971, V246, P6511 HCAPLUS
(22) Mayhew, M; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P922
(23) Miller, J; Experiments in molecular genetics 1972
(24) Neidhardt, F; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P1310
(25) Neidhardt, F; Physiology of the bacterial cell: a molecular approach 1990
(26) O'Farrell, P; J Biol chem 1975, V250, P4007 HCAPLUS
(27) Petersen, J; Nucleic Acids Res 1986, V14, P9631 HCAPLUS
(28) Pittard, A; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P458
(29) Potsma, P; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P1149
(30) Reznikoff, W; The operon 1978, P221 HCAPLUS
(31) Richmond, C; Nucleic Acids Res 1999, V27, P3821 HCAPLUS
(32) Riley, M; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V2, P2118
(33) Roberts, R; Studies of biosynthesis in Escherichia coli publication 1963, 607
(34) Tao, H; J Bacteriol 1999, V181, P6425 HCAPLUS
(35) Umbarger, H; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V1, P442
(36) VanBogelen, R; Escherichia coli and Salmonella: cellular and molecular biology 2nd ed 1996, V2, P2067
(37) VanBogelen, R; J Bacteriol 1987, V169, P26 HCAPLUS
(38) Van Dyk, T; Methods Mol Biol 1998, V102, P85 HCAPLUS
(39) Wedicka, L; Nat Biotechnol 1997, V15, P1359
(40) Wittenbach, V; Biosynthesis and molecular regulation of amino acids in plants 1992, P69

L108 ANSWER 2 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:859179 HCAPLUS
TI Recovery of Developmentally Defined Gene Sets from **High-Density** cDNA **Macroarrays**
AU Rast, Jonathan P.; Amore, Gabriele; Calestani, Cristina; Livi, Carolina B.; Ransick, Andrew; Davidson, Eric H.
CS Division of Biology 156-29, California Institute of Technology, Pasadena, CA, 91125, USA
SO Dev. Biol. (2000), 228(2), 270-286
CODEN: DEBIAO; ISSN: 0012-1606
PB Academic Press
DT Journal
LA English
CC 3 (Biochemical Genetics)
AB New technologies for isolating differentially expressed genes from large

arrayed cDNA libraries are reported. These methods can be used to identify genes that lie downstream of developmentally important **transcription** factors and genes that are expressed in specific tissues, processes, or stages of embryonic development. Though developed for the study of gene expression during the early embryogenesis of the sea urchin Strongylocentrotus purpuratus, these technologies can be applied generally. **Hybridization** parameters were detd. for the reaction of complex cDNA probes to cDNA libraries carried on six nylon filters, each contg. duplicate spots from 18,432 bacterial clones (**macroarrays**). These libraries are of sufficient size to include nearly all genes expressed in the embryo. The screening strategy we have devised is designed to overcome inherent sensitivity limitations of **macroarray hybridization** and thus to isolate differentially expressed genes that are represented only by low-prevalence mRNAs. To this end, we have developed improved methods for the amplification of cDNA from small amts. of tissue (as little as .apprx.300 sea urchin embryos, or 2 .times. 105 cells, or about 10 ng of mRNA) and for the differential enhancement of probe **sequence** concn. by subtractive **hybridization**. Quant. anal. of **macroarray hybridization** shows that these probes now suffice for detection of differentially expressed mRNAs down to a level below five mols. per av. embryo cell. (c) 2000 Academic Press.

RE.CNT 30

RE

(1) Arnone, M; Development 1997, V124, P4649 HCAPLUS
(2) Britten, R; Methods Enzymol 1974, V29, P363 HCAPLUS
(3) Brown, P; Nat Genet 1999, V21, P33 HCAPLUS
(4) Clark, M; Methods Enzymol 1999, V303, P205 HCAPLUS
(5) Davidson, E; Gene Activity in Early Development 1986
(6) Flytzanis, C; Dev Biol 1982, V91, P27 HCAPLUS
(7) Galau, G; Proc Natl Acad Sci USA 1977, V74, P1020 HCAPLUS
(8) Gubler, U; Gene 1983, V25, P263 HCAPLUS
(9) Hampson, I; Nucleic Acids Res 1996, V24, P4832 HCAPLUS
(10) Hough-Evans, B; Dev Biol 1988, V129, P198 HCAPLUS
(11) Kacharmina, J; Methods Enzymol 1999, V303, P3 HCAPLUS
(12) Killian, C; Dev Biol 1989, V133, P148 HCAPLUS
(13) Kohne, D; Biochemistry 1977, V16, P5329 HCAPLUS
(14) Lasky, L; Proc Natl Acad Sci USA 1980, V77, P5317 HCAPLUS
(15) Lee, J; J Mol Biol 1986, V188, P173 HCAPLUS
(16) Lee, Y; Dev Growth Differ 1999, V41, P303 HCAPLUS
(17) Lee, Y; Development 1999, V126, P3857 HCAPLUS
(18) Lipshutz, R; Nat Genet 1999, V21, P20 HCAPLUS
(19) Livant, D; Development 1991, V113, P385 HCAPLUS
(20) Maier, E; J Biotechnol 1994, V35, P191 HCAPLUS
(21) McClay, D; Methods Cell Biol 1986, V27, P309 MEDLINE
(22) McMahon, A; Dev Biol 1985, V108, P420 HCAPLUS
(23) Nemer, M; Dev Biol 1991, V145, P255 HCAPLUS
(24) Nizetic, D; Nucleic Acids Res 1991, V19, P182 HCAPLUS
(25) Peterson, K; Dev Biol 1999, V207, P419 HCAPLUS
(26) Phillips, J; Methods: Companion Methods Enzymol 1996, V10, P283 HCAPLUS
(27) Poustka, A; Genomics 1999, V59, P122 HCAPLUS
(28) Sagerstrom, C; Annu Rev Biochem 1997, V66, P751 HCAPLUS
(29) Siebert, P; Nucleic Acids Res 1995, V23, P1087 HCAPLUS
(30) Sive, H; Nucleic Acids Res 1988, V16, P10937 HCAPLUS

L108 ANSWER 3 OF 13 HCAPLUS COPYRIGHT 2001 ACS

AN 2000:834957 HCAPLUS

TI Rapid cloning of metK encoding methionine adenosyltransferase from Corynebacterium glutamicum by screening a **genomic** library on a **high density** colony-**array**

AU Grossmann, K.; Herbster, K.; Mack, M.
CS BASF-LYNX Bioscience AG, Heidelberg, 69120, Germany

SO FEMS Microbiol. Lett. (2000), 193(1), 99-103
CODEN: FMLED7; ISSN: 0378-1097
PB Elsevier Science B.V.
DT Journal

LA English
CC 3 (Biochemical Genetics)
AB The genes SAM1 and SAM2 encoding the two different methionine adenosyltransferases (EC 2.5.1.6) in Saccharomyces cerevisiae were used as templates to generate specific DNA-probes. This heterologous mixt. of DNA-probes was **hybridized** under low stringency **hybridization** conditions to a Corynebacterium glutamicum colony-**array** representing the complete **genome**. Subsequently, one **genomic** fragment was isolated which contained the C. glutamicum methionine adenosyltransferase gene metK (1.224 kb). When overproduced in Escherichia coli, MetK (44.2 kDa) of C. glutamicum had methionine adenosyltransferase activity. In addn., overexpression of metK in C. glutamicum led to an increased intracellular S-adenosylmethionine concn. The metK **transcript** was detected by reverse **transcription** PCR in C. glutamicum cells in the exponential growth phase but not in the stationary phase.
RE.CNT 19
RE
(1) Altenbuchner, J; Mol Gen Genet 1984, V195, P134 HCAPLUS
(2) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS
(3) Bathe, B; Mol Gen Genet 1996, V252, P255 HCAPLUS
(4) Cantoni, G; The Biochemistry of Adenosylmethionine 1977, P557 HCAPLUS
(5) Cremer, J; Mol Gen Genet 1999, V220, P478
(6) Furste, J; Gene 1986, V48, P119 MEDLINE
(7) Hatakeyama, K; JP 22-7287 A1 1995
(8) Keilhauer, C; J Bacteriol 1993, V175, P5595 HCAPLUS
(9) Markham, G; J Biol Chem 1980, V255, P9082 HCAPLUS
(10) Markham, G; J Biol Chem 1984, V259, P14505 HCAPLUS
(11) Mautino, M; Gene 1996, V170, P155 HCAPLUS
(12) Miller, J; A Laboratory Manual and Handbook for Escherichia coli and Related Bacteria 1992
(13) Sambrook, J; Molecular Cloning: A Laboratory Manual 1989
(14) Sherman, F; Methods in Yeast Genetics: A Laboratory Manual 1979
(15) Thierbach, G; Appl Microbiol Biotechnol 1988, V29, P356 HCAPLUS
(16) Thomas, D; J Biol Chem 1987, V262, P16704 HCAPLUS
(17) Thomas, D; Mol Cell Biol 1988, V8, P5132 HCAPLUS
(18) Vente, A; Nature Genet 1999, V22, P22 HCAPLUS
(19) Yocum, R; J Bacteriol 1996, V178, P4604 HCAPLUS

L108 ANSWER 4 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:651328 HCAPLUS
DN 133:331693
TI Laser capture microdissection-generated target sample for **high-density** oligonucleotide **array hybridization**.
AU Ohyama, H.; Zhang, X.; Kohno, Y.; Alevizos, I.; Posner, M.; Wong, D. T.; Todd, R.
CS Harvard School of Dental Medicine, Boston, MA, USA
SO BioTechniques (2000), 29(3), 530-534,536
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
CC 9-16 (Biochemical Methods)
Section cross-reference(s): 3, 6, 14
AB Current advances in biomol. technol. allow precise genetic fingerprinting of specific cells responsible for the pathogenesis of human diseases. This study demonstrates the feasibility of generating target samples from laser capture microdissection (LCM) tissues suitable for **hybridization** of high-d. oligonucleotide **arrays** for gene expression profiling. RNA was successfully isolated by LCM from three paired specimens of oral cancer and linearly amplified using T7 RNA polymerase. Evaluation of the cDNA revealed that five of five cellular maintenance **transcripts** are detected. Biotinylated cRNA was generated and **hybridized** to the human Test 1 **GeneChip** probe **arrays**, which demonstrated that the RNA is of sufficient quality and integrity to warrant further anal. Subsequent

hybridization of the samples to the HuGenFL **GeneChip** probe **arrays** revealed that 26.5%-33.0% of the approx. 7000 represented genes are expressed in each of the six samples. These results demonstrate that LCM-generated tissues can generate sufficient quality cRNA for high-d. oligonucleotide **microarray** anal., an important step in detg. comprehensive gene expression profiling using this high-throughput technol.

ST RNA tongue cancer **hybridization** laser capture microdissection

IT Gene
(expression; laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

IT Nucleic acid **hybridization**
(laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

IT RNA
RL: ANT (Analyte); BPR (Biological process); PUR (Purification or recovery); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)
(laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

IT Lasers
(laser capture microdissection; laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

IT Tongue
(neoplasm; laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

IT Tongue
(squamous cell carcinoma; laser capture microdissection-generated target sample for high-d. oligonucleotide **array hybridization**)

RE.CNT 9

RE
(1) Emmert-Buck, M; Science 1996, V274, P998 HCAPLUS
(2) Katcharmina, J; Methods Enzymol 1999, V303, P3
(3) Lockhart, D; Nat Biotechnol 1996, V14, P1675 HCAPLUS
(4) Luo, L; Nat Med 1999, V5, P117 HCAPLUS
(5) Mahdevapa, M; Nat Biotechnol 1999, V17, P1134
(6) Saizieu, A; Nat Biotechnol 1998, V16, P45
(7) Simone, N; Trends Genet 1998, V14, P272 HCAPLUS
(8) Suarez-Quian, C; BioTechniques 1999, V26, P328 HCAPLUS
(9) Wodicka, L; Nat Biotechnol 1997, V15, P1359 HCAPLUS

L108 ANSWER 5 OF 13 HCAPLUS COPYRIGHT 2001 ACS

AN 2000:525073 HCAPLUS

DN 134:13923

TI Global analysis of **transcription** kinetics during competence development in Streptococcus pneumoniae using **high density** DNA **arrays**

AU Rimini, Rebecca; Jansson, Birger; Feger, Georg; Roberts, Tracy C.; De Francesco, Massimo; Gozzi, Alessandro; Faggioni, Federico; Domenici, Enrico; Wallace, Donald M.; Frandsen, Niels; Polissi, Alessandra

CS Department of Microbiology, Glaxo Wellcome S.p.A., Verona, 37100, Italy

SO Mol. Microbiol. (2000), 36(6), 1279-1292
CODEN: MOMIEE; ISSN: 0950-382X

PB Blackwell Science Ltd.

DT Journal

LA English

CC 3-4 (Biochemical Genetics)
Section cross-reference(s): 10

AB The kinetics of global changes in **transcription** patterns during competence development in Streptococcus pneumoniae was analyzed with high-d. **arrays**. Four thousand three hundred and one clones of a S. pneumoniae library, covering almost the entire **genome**, were amplified by PCR and gridden at high d. onto nylon membranes. Competence was induced by the addn. of CSP (competence stimulating peptide) to S.

pneumoniae cultures grown to the early exponential phase. RNA was extd. from samples at 5 min intervals (for a period of 30 min) after the addn. of CSP. Radiolabeled cDNA was generated from isolated total RNA by random priming and the probes were **hybridized** to identical high-d. **arrays**. Genes whose **transcription** was induced or repressed during competence were identified. Most of the genes previously known to be competence induced were detected together with several novel genes that all displayed the characteristic transient kinetics of competence-induced genes. Among the newly identified genes many have suggested functions compatible with roles in genetic transformation. Some of them may represent new members of the early or late competence regulons showing competence specific consensus **sequences** in their promoter regions. Northern expts. and mutational anal. were used to confirm some of the results.

ST Streptococcus gene **transcription** competence development; DNA **array high density** Streptococcus gene **transcription** competence development

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(BBO843; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(Hl1647; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(cbp3; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(cbp6; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Transformation, genetic
(competence for; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(competence induced; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(dnaK; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(dpnMA; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Development, microbial
Streptococcus pneumoniae
Transcription, genetic
(global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Promoter (genetic element)
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BIOL (Biological study); PROC (Process)
(global anal. of **transcription** kinetics during competence

development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(hemN; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(iga; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(lcn972; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(orf190; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(orf2; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(orf62/orf51; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(pflC; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(yhaP; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(yhaQ; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(ypjC; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(ysxA; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(yueJ; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA **arrays**)

IT Gene, microbial
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(yulF; global anal. of **transcription** kinetics during competence development in Streptococcus pneumoniae using high d. DNA

arrays)
RE.CNT 53
RE
(1) Alloing, G; Mol Microbiol 1998, V29, P75 HCAPLUS
(2) Altschul, F; Nucleic Acids Res 1997, V25, P3389
(3) Briles, D; Rev Infect Dis 1988, V10, PS372 HCAPLUS
(4) Campbell, E; Mol Microbiol 1998, V27, P929 HCAPLUS
(5) Chu, S; Science 1998, V282, P699 HCAPLUS
(6) Chuang, S; J Bacteriol 1993, V175, P2026 HCAPLUS
(7) Claverys, J; Gene 1995, V164, P123 HCAPLUS
(8) Claverys, J; Mol Microbiol 1998, V29, P1126 HCAPLUS
(9) Claverys, J; Mol Microbiol 2000, V35, P251 HCAPLUS
(10) de Saizieu, A; Nature Biotechnol 1998, V16, P45 HCAPLUS
(11) Dijkstra, A; J Bacteriol 1996, V176, P5555
(12) Dubnau, D; Gene 1997, V192, P191 HCAPLUS
(13) Felzenszwalb, I; Radiat Res 1986, V106, P166 HCAPLUS
(14) Gasc, A; J Bacteriol 1991, V173, P7361 HCAPLUS
(15) Georgopoulos, C; Annu Rev Cell Biol 1993, V9, P601 HCAPLUS
(16) Giammarinaro, P; Microbiology 1999, V145, P1859 HCAPLUS
(17) Guenzi, E; Mol Microbiol 1994, V12, P505 HCAPLUS
(18) Hartl, F; Nature 1996, V381, P571 HCAPLUS
(19) Havarstein, L; Mol Microbiol 1996, V21, P863 HCAPLUS
(20) Havarstein, L; Proc Natl Acad Sci USA 1995, V92, P11140 MEDLINE
(21) Higgins, C; Annu Rev Cell Biol 1992, V8, P67 HCAPLUS
(22) Homuth, G; Microbiology 1996, V142, P1641 HCAPLUS
(23) Hui, F; Gene 1995, V153, P25 HCAPLUS
(24) Hui, F; J Bacteriol 1991, V173, P372 HCAPLUS
(25) Jelinsky, S; Proc Natl Acad Sci USA 1999, V96, P1486 HCAPLUS
(26) Kleerebezem, M; Mol Microbiol 1997, V24, P895 HCAPLUS
(27) Lacks, S; Gene 1995, V157, P209 HCAPLUS
(28) Lacks, S; Genetic Recombination 1988, P43
(29) Lacks, S; Transport of Molecules Across Microbial Membranes, Symposia of the Society for General Microbiology 1999, P138 HCAPLUS
(30) Lee, M; Appl Environ Microbiol 1999, V65, P1883 HCAPLUS
(31) Lee, M; J Bacteriol 1999, V181, P5004 HCAPLUS
(32) Martin, B; Mol Microbiol 1995, V15, P367 HCAPLUS
(33) Morrison, D; Nature 1979, V282, P215 HCAPLUS
(34) Mortier-Barriere, I; Mol Microbiol 1998, V27, P159 HCAPLUS
(35) Munoz, R; J Bacteriol 1995, V177, P4166 HCAPLUS
(36) Novak, R; J Bacteriol 1999, V181, P1126 HCAPLUS
(37) Okaichi, K; Photochem Photobiol 1995, V61, P281 HCAPLUS
(38) Pearce, B; J Bacteriol 1995, V177, P86 HCAPLUS
(39) Pestova, E; J Bacteriol 1998, V180, P2701 HCAPLUS
(40) Pestova, E; Mol Microbiol 1996, V21, P853 HCAPLUS
(41) Pozzi, G; J Bacteriol 1996, V178, P6087 HCAPLUS
(42) Richmond, C; Nucleic Acids Res 1999, V27, P3821 HCAPLUS
(43) Rockabrand, D; J Bacteriol 1998, V180, P846 HCAPLUS
(44) Roedel, W; Eur J Biochem 1988, V177, P153 HCAPLUS
(45) Ronda, C; Eur J Biochem 1987, V164, P621 HCAPLUS
(46) Rosenow, C; Mol Microbiol 1997, V25, P819 HCAPLUS
(47) Sambrook, K; Molecular Cloning: a laboratory Manual, 2nd edn 1989
(48) Saveson, C; Genetics 1999, V152, P5 HCAPLUS
(49) Schena, M; Science 1995, V270, P467 HCAPLUS
(50) Teter, S; Cell 1999, V97, P755 HCAPLUS
(51) Tomasz, A; Proc Natl Acad Sci USA 1964, V51, P480 MEDLINE
(52) Ween, O; Mol Microbiol 1999, V33, P817 HCAPLUS
(53) Wodicka, L; Nature Biotechnol 1997, V15, P1359 HCAPLUS

L108 ANSWER 6 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:50306 HCAPLUS
DN 132:318370
TI Analysis of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and **high-density** cDNA **arrays**
AU Zanders, E. D.; Goulden, M. G.; Kennedy, T. C.; Kempsell, K. E.
CS Immunopathology Unit, Glaxo-Wellcome Research and Development, Stevenage,

UK
SO J. Immunol. Methods (2000), 233(1-2), 131-140
CODEN: JIMMBG; ISSN: 0022-1759
PB Elsevier Science B.V.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 13, 15
AB Subtractive **hybridization** of cDNAs generated from synovial RNA which had been isolated from patients with rheumatoid arthritis (RA) or normal controls was used in conjunction with high-d. **array hybridization** to identify genes of immunol. interest. The method was designed to detect gene expression in small needle biopsy specimens by means of a prior amplification of nanogram amts. of total RNA to full-length cDNA using PCR. The latter was cut with Rsa I, ligated with adapters, **hybridized** with unmodified driver cDNA, and subjected to suppression subtraction PCR. Differentially expressed products were cloned into E. coli and picked into 384 well plates. Inserts were obtained by PCR across the multiple cloning site, and the products **arrayed** at high d. on nylon filters. The subtracted cDNAs were also labeled by random priming for use as probes for library screening. The libraries chosen were the subtracted one described above and a set of 45,000 ESTs from the I.M.A.G.E consortium. Clones showing pos. **hybridization** were identified by **sequence** anal. and homol. searching. The results showed that the subtracted **hybridization** approach could identify many gene fragments expressed at different levels, the most abundant being Igs and HLA-DR. The expression profile was characteristic of macrophage, B cell and plasma cell infiltration with evidence of interferon induction. In addn., a significant no. of **sequences** without matches in the nucleotide databases were obtained, this demonstrates the utility of the method in finding novel gene fragments for further characterization as potential members of the immune system. Although RA was studied here, the technol. is applicable to any disease process even in cases where amts. of tissue may be limited.
ST rheumatoid arthritis immune system gene expression subtractive **hybridization** PCR; subtractive **hybridization** cDNA **array** rheumatoid arthritis immune gene expression
IT Gene, animal
RL: ANT (Analyte); ANST (Analytical study)
(HLA-DR; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT Immune system
PCR (polymerase chain reaction)
Reverse **transcription**
Rheumatoid arthritis
(anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT EST (expressed **sequence** tag)
RL: ANT (Analyte); ANST (Analytical study)
(anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT cDNA
RL: ANT (Analyte); BUU (Biological use, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT Gene, animal
RL: ANT (Analyte); ANST (Analytical study)
(for Ig; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)

IT mRNA
RL: ANT (Analyte); ANST (Analytical study)
(gene expression; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT Nucleic acid **hybridization**
(high-d. **array**; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT Gene, animal
RL: ANT (Analyte); ANST (Analytical study)
(involved in immune system; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**)
IT Nucleic acid **hybridization**
(subtractive, selective suppression PCR; anal. of immune system gene expression in small rheumatoid arthritis biopsies using a combination of subtractive **hybridization** and high-d. cDNA **arrays**
)
RE.CNT 23
RE
(1) Adams, M; Nature 1995, V377, P3 HCAPLUS
(2) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(3) Brady, G; Methods Enzymol 1993, V225, P611 HCAPLUS
(4) Chomczynski, P; Anal Biochem 1987, V162, P156 HCAPLUS
(5) Edwards, J; Mechanisms and Models in Rheumatoid Arthritis 1995, P133
(6) Elliot, M; Lancet 1994, V344, P1105
(7) Feldmann, M; Cell 1996, V85, P307 HCAPLUS
(8) Firestein, G; Arthritis Rheum 1991, V34, P1094 MEDLINE
(9) Gurskaya, N; Anal Biochem 1996, V240, P90 HCAPLUS
(10) Heller, R; Proc Natl Acad Sci U S A 1997, V94, P2150 HCAPLUS
(11) Hubank, M; Nucleic Acids Res 1994, V22, P5640 HCAPLUS
(12) Kotake, S; Proc Assoc Am Physicians 1997, V109, P286 HCAPLUS
(13) Lennon, G; Genomics 1996, V33, P151 HCAPLUS
(14) Liang, P; Science 1992, V257, P967 HCAPLUS
(15) Mangasser-Stephan, K; Biochem Biophys Res Comm 1997, V234, P153 HCAPLUS
(16) Panayi, G; Br J Rheumatol 1993, V32, P4
(17) Ritchlin, C; Scand J Immunol 1994, V40, P292 HCAPLUS
(18) Schena, M; Science 1995, V270, P467 HCAPLUS
(19) Seki, T; Arthritis Rheum 1998, V41, P1356 HCAPLUS
(20) Trower, M; Microb Comp Genomics 1997, V12, P236
(21) Trower, M; Nucleic Acids Res 1995, V23, P2348 HCAPLUS
(22) Winchester, R; Clin Exp Rheumatol 1993, V11, PS87
(23) Zvaifler, N; Arthritis Rheum 1994, V37, P783 HCAPLUS

L108 ANSWER 7 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:761296 HCAPLUS
DN 132:161820
TI Negative selection: a method for obtaining low-abundance cDNAs using **high-density** cDNA clone **arrays**
AU Nelson, P. S.; Hawkins, V.; Schummer, M.; Bumgarner, R.; Ng, W.-L.; Ideker, T.; Ferguson, C.; Hood, L.
CS Department of Molecular Biotechnology, University of Washington, Seattle, WA, USA
SO Genet. Anal.: Biomol. Eng. (1999), 15(6), 209-215
CODEN: GEANF4; ISSN: 1050-3862
PB Elsevier Science B.V.
DT Journal
LA English
CC 3-2 (Biochemical Genetics)
AB The identification of the entire complement of genes expressed in a cell, tissue, or organism provides a framework for understanding biol. properties and establishes a tool set for subsequent functional studies. The large-scale **sequencing** of randomly selected clones from cDNA libraries has been successfully employed as a method for identifying a large fraction of these expressed genes. However, this approach is

limited by the inherent redundancy of cellular **transcripts** reflecting widely variant levels of gene **transcription**. As a result, a high percentage of **transcript** duplications are encountered as the no. of **sequenced** clones accrues. To address this problem, the authors have developed a neg. **hybridization** selection method that employs the **hybridization** of complex cDNA probes to high-d. **arrays** of cDNA clones and the subsequent selection of clones with a null or low **hybridization** signal. This approach was applied to a cDNA library constructed from normal human prostate tissue and resulted in the redn. of highly expressed prostate cDNAs from 6.8 to 0.57% with an overall decline in clone redundancy from 33 to 11%. The selected clones also reflected a more diverse cDNA population, with 89% of the clones representing distinctly different cDNAs compared with 67% of the randomly selected clones. This method compares favorably with cDNA library re-assocn. normalization approaches and offers several distinct advantages, including the flexibility to use previously prepd. libraries, and the ability to employ an iterative screening approach for continued accrual of cDNAs representing rare **transcripts**.

ST cDNA cloning neg **hybridization** selection method

IT Nucleic acid **hybridization**
(DNA-DNA; neg. **hybridization** selection method for obtaining low-abundance cDNAs using high-d. cDNA clone **arrays**)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(cDNA; neg. **hybridization** selection method for obtaining low-abundance cDNAs using high-d. cDNA clone **arrays**)

IT Molecular cloning
cDNA library
(neg. **hybridization** selection method for obtaining low-abundance cDNAs using high-d. cDNA clone **arrays**)

IT cDNA
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(neg. **hybridization** selection method for obtaining low-abundance cDNAs using high-d. cDNA clone **arrays**)

IT EST (expressed **sequence** tag)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(neg. **hybridization** selection method for obtaining low-abundance cDNAs using high-d. cDNA clone **arrays**)

RE.CNT 23

RE

(1) Adams, M; Nature 1995, V377(Suppl 28), P3
(2) Adams, M; Science 1991, V252, P1651 HCAPLUS
(3) Altschul, S; J Mol Biol 1990, V215, P403 HCAPLUS
(4) Bishop, J; Nature 1974, V250, P199 HCAPLUS
(5) Bonaldo, M; Genome Res 1996, V6, P791 HCAPLUS
(6) Gress, T; Mammalian Genome 1992, V3, P359
(7) Gurskaya, N; Anal Biochem 1996, V240(1), P90 HCAPLUS
(8) Hoog, C; Nucleic Acids Res 1991, V19(22), P6123 MEDLINE
(9) Huang, X; Genomics 1992, V14(1), P18 HCAPLUS
(10) Ko, M; Nucleic Acids Res 1990, V18, P5705 HCAPLUS
(11) Lilja, H; J Biol Chem 1989, V264(3), P1894 HCAPLUS
(12) Nelson, P; Genomics 1998, V47(1), P12 HCAPLUS
(13) Nguyen, C; Genomics 1995, V29, P207 HCAPLUS
(14) Nizetic, D; Nucleic Acids Res 1991, V19, P182 HCAPLUS
(15) Orr, S; Proc Natl Acad Sci USA 1994, V91(25), P11869 HCAPLUS
(16) Schena, M; Science 1995, V270, P467 HCAPLUS
(17) Schummer, M; Biotechniques 1997, V23, P1087 HCAPLUS
(18) Soares, M; Proc Natl Acad Sci USA 1994, V91, P9228 HCAPLUS
(19) Takahashi, N; Genomics 1994, V23(1), P202 HCAPLUS
(20) Wallace, D; Human Gene Mapping 1995, P910
(21) Wang, K; anal Biochem 1995, V226, P85 HCAPLUS
(22) Wodicka, L; Nat Biotechnol 1997, V15, P1359 HCAPLUS
(23) Zhang, L; Science 1997, V276, P1268 HCAPLUS

L108 ANSWER 8 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:720972 HCAPLUS
DN 132:45521
TI In the laboratory: A **high-density** probe **array** sample preparation method using 10- to 100-fold fewer cells
AU Mahadevappa, Mamatha; Warrington, Janet A.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Nat. Biotechnol. (1999), 17(11), 1134-1136
CODEN: NABIF9; ISSN: 1087-0156
PB Nature America
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
AB Poly(A) prepn. methods generally require large amts. of starting material because of sample loss during isolation. In an effort to reduce the amt. of required starting material, we describe a method that eliminates the poly(A) extn. step and uses total RNA as the template in a cDNA reaction. We compare this method with the std. poly(A) RNA method and report results obtained from **hybridizing** samples prepd. from 50,000, 100,000, and 200,000 cells. Sample prepn. method begins with total RNA extn. from cells or tissues. Double-stranded cDNA synthesis is followed by in vitro **transcription** for amplification and labeling of targets. Labeled target is fragmented and **hybridized** to **GeneChip** **arrays** overnight. After washing and staining, **arrays** are scanned. Comparable expression results were obtained from **hybridizing** samples prepd. by the total RNA and poly(A) RNA methods. The total RNA method requires substantially less starting material to achieve sensitivity similar to that of the poly(A) RNA method. These expts. demonstrate that with limited amts. of starting material (250 pg of tissue, 50,000 cells), we are able to obtain 75-80% of the information obtained with six times as many cells (300,000) or with 100 times as many cells as recommended by the current poly(A) method. Although this method is efficient, it does not solve the problem of measuring expression from one or a few cells; however, it does provide a simple means for prepg. samples from tens of thousands of cells without using PCR.
ST probe **array** **GeneChip** RNA sample prepn gene expression detn
IT Recombination, genetic
(amplification; high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT Biotechnology
(**biochips**, **GeneChip**; high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT Gene
(expression; high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT Cell
Nucleic acid **hybridization**
Sample preparation
Staining, biological
(high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT cDNA
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT Probes (nucleic acid)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)
IT RNA
RL: BSU (Biological study, unclassified); PUR (Purification or recovery);

BIOL (Biological study); PREP (Preparation)
(high-d. probe **array** sample prepn. method using 10- to 100-fold fewer cells for gene expression measuring)

RE.CNT 17
RE
(1) Affymetrix Inc; Eukaryotic expression analysis target preparation product enclosure 1998
(2) Berne, R; Physiology 2nd Edn 1988
(3) Choi, S; J Biochem Mol Biol 1996, V29, P272 HCAPLUS
(4) Endege, W; BioTechniques 1999, V26, P542 HCAPLUS
(5) Fodor, S; Science 1991, V251, P767 HCAPLUS
(6) Fodor, S; Science 1993, V364, P555 MEDLINE
(7) Lander, E; Nat Genet 1999, V21(Suppl), P3
(8) Lee, P; Proc Natl Acad Sci 1996, V93, P10366 HCAPLUS
(9) Lockhart, D; Nat Biotechnol 1996, V14, P1675 HCAPLUS
(10) Phillips, J; Methods: a companion to methods in enzymology 1996, V10, P283 HCAPLUS
(11) Rappolee, D; J Cell Biochem 1989, V39, P1 HCAPLUS
(12) Sambrook, J; Molecular cloning: a laboratory manual 2nd Edn 1989, V3
(13) Schena, M; Proc Natl Acad Sci 1996, V93, P10614 HCAPLUS
(14) Schena, M; Science 1995, V270, P467 HCAPLUS
(15) Van Gelder, R; Proc Natl Acad Sci 1990, V87, P1663 HCAPLUS
(16) Velculescu, E; Science 1995, V270, P484
(17) Wodicka, L; Nat Biotechnol 1997, V15, P1359 HCAPLUS

L108 ANSWER 9 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:451363 HCAPLUS
DN 131:69264
TI Methods for screening interacting molecules by direct **hybridization** of nucleic acids to **high-density** oligonucleotide **arrays**
IN Legrain, Pierre; Fromont-Racine, Micheline; Cho, Raymond; Davis, Ronald; Lockhart, D.; Wodicka, L.
PA Institut Pasteur, Fr.; Stanford University; Affymetrix
SO PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-10
ICS C12Q001-68
CC 3-1 (Biochemical Genetics)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9935256	A1	19990715	WO 1999-IB48	19990106
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9917780	A1	19990726	AU 1999-17780	19990106
PRAI	US 1998-3335	19980106			
	US 1998-154972	19980917			
	WO 1999-IB48	19990106			

AB This invention relates to methods for the identification of nucleic acids by direct **hybridization** to high-d. oligonucleotide **arrays**. The methods of this invention comprise the steps of: (a) screening a DNA library, such as an S. cerevisiae **genomic** DNA library, by performing a double **hybrid** screening method with a recombinant vector contg. a DNA insert encoding a candidate protein of interest and then selecting the clones from the DNA library that code for proteins that interact with the candidate protein of interest; and (b)

hybridizing the DNA inserts contained in the clones that have been selected in step (a) using an oligonucleotide probe matrix wherein the probe locations on the host **genome** cover all of the coding **sequences**, detg. the **hybridization** location and consequently, the gene coding for a specific protein that interacts with the candidate protein of interest in the double **hybrid** screening system. One of the most important features of the **hybridized** DNA **arrays** utilized in the screening methods of this invention is that the DNA **arrays** allow, in a one-step method, mapping of all the potential polypeptides interacting with a given defined polypeptide in a forward two-**hybrid** method, or inhibiting the interaction between two defined polypeptides in a reverse two-**hybrid** method. Thus, the **hybridization** pattern of oligo- or polynucleotides coding for the interactor polypeptides identify the whole set of polypeptides of interest. In contrast, the prior art technique of systematic **sequencing** of every selected polynucleotide identified only individual interactor coding **sequences** and did not provide any understanding of the global interaction possibilities.

ST DNA **sequence** analysis oligonucleotide **array** protein interaction

IT Nucleic acid amplification (method)
(DNA; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT Gene, microbial
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(GAL4, **transcriptional** activator of; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT Promoter (genetic element)
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(bacteriophage T7; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT Eukaryote (Eukaryotae)
Prokaryote
(detection of interacting mols. in; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(immobilized; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT DNA **sequence** analysis
Nucleic acid **hybridization**
(methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT Saccharomyces cerevisiae
(screening of the DNA library of; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT **Genomic** library
(screening of; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT 9012-90-2, DNA polymerase
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(bacteriophage; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)

IT 9014-24-8, RNA polymerase 9068-38-6, Reverse **transcriptase**
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical

study); USES (Uses)
(incubation of amplified DNA with; methods for screening interacting mols. by direct **hybridization** of nucleic acids to high-d. oligonucleotide **arrays**)
RE.CNT 10
RE
(1) Cho; PNAS 1998, V95, P3752 HCAPLUS
(2) Cronin, M; WO 9743450 A 1997 HCAPLUS
(3) Fields, S; Trends in Genetics 1994, V10(8), P286 HCAPLUS
(4) Fromont-Racine; Nature Genetics 1997, V16, P277 HCAPLUS
(5) Lashkari; PNAS 1997, V94, P8945 HCAPLUS
(6) Lecrenier; Bioessays 1998, V20(1), P1 MEDLINE
(7) Oliver; Current Opinion in Genetics & Development 1997, V7, P405
(8) Onyx Pharma Inc; WO 9526400 A 1995 HCAPLUS
(9) Shoemaker, D; Nature Genetics 1996, V14(4), P450 HCAPLUS
(10) Wodicka; Nature Biotechnology 1997, V15, P1359 HCAPLUS

L108 ANSWER 10 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:746377 HCAPLUS
DN 130:120100
TI Enhanced **high density** oligonucleotide **array** -based **sequence** analysis using modified nucleoside triphosphates
AU Hacia, Joseph G.; Woski, Stephen A.; Fidanza, Jacqueline; Edgemon, Keith; Hunt, Nathaniel; McGall, Glenn; Fodor, Stephen P. A.; Collins, Francis S.
CS National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 20892-2152, USA
SO Nucleic Acids Res. (1998), 26(21), 4975-4982
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB Pairs of high d. oligonucleotide **arrays** (DNA chips) consisting of >96,000 oligonucleotides were designed to screen the entire 5.53 kb coding region of the hereditary breast and ovarian cancer BRCA1 gene for all possible **sequence** changes in the homozygous and heterozygous states. Single-stranded RNA targets were generated by PCR amplification of individual BRCA1 exons using primers contg. T3 and T7 RNA polymerase promoter tails followed by in vitro **transcription** and partial fragmentation reactions. Fluorescent **hybridization** signals from targets contg. the four natural bases to >5592 different fully complementary 25mer oligonucleotide probes on the chip varied over two orders of magnitude. To examine the thermodn. contribution of rU.cntdot.dA and rA.cntdot.dT target.cntdot.probe base pairs to this variability, modified uridine [5-methyluridine and 5-(1-propynyl)-uridine] and modified adenosine (2,6-diaminopurine riboside) 5'-triphosphates were incorporated into BRCA1 targets. **Hybridization** specificity was assessed based upon **hybridization** signals from >33 200 probes contg. centrally localized single base pair mismatches relative to target **sequence**. Targets contg. 5-methyluridine displayed promising localized enhancements in **hybridization** signal, esp. in pyrimidine-rich target tracts, while maintaining single nucleotide mismatch **hybridization** specificities comparable with those of unmodified targets.
ST oligonucleotide **array sequence** analysis gene BRCA1 modified nucleoside triphosphate
IT DNA **sequence** analysis
DNA-RNA **hybridization**
(DNA chip; enhanced high d. oligonucleotide **array**-based **sequence** anal. using modified nucleoside triphosphates)
IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(T3 and T7 RNA polymerase promoter tails in primers for BRCA1 exon amplification; enhanced high d. oligonucleotide **array**-based

sequence anal. of BRCA1 using modified nucleoside triphosphates)

IT Exon (genetic element)
RL: ANT (Analyte); BPN (Biosynthetic preparation); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amplification of BRCA1 exons; enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT Oligodeoxyribonucleotides
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(**arrays**; enhanced high d. oligonucleotide **array**-based **sequence** anal. using modified nucleoside triphosphates)

IT Genetic diagnosis
(enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT BRCA1 gene (animal)
RL: ANT (Analyte); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT **Transcription** (genetic)
(in vitro **transcription** of **hybridization** target using modified nucleoside triphosphate; enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT Hydrogen bond
(of modified pyrimidine and purine bases; enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT 219778-22-0 219778-23-1 219778-27-5 219778-28-6 219778-29-7
219778-30-0 219778-31-1 219778-32-2 219778-33-3 219778-34-4
219778-36-6 219778-37-7 219778-38-8 219778-39-9 219778-41-3
219778-42-4 219778-45-7 219778-46-8 219778-47-9 219778-49-1
219778-50-4 219778-51-5 219778-53-7 219778-54-8 219778-55-9
219778-56-0 219778-57-1 219778-58-2 219778-59-3 219778-60-6
219778-61-7 219778-62-8 219778-63-9 219778-64-0 219778-65-1
219778-66-2 219778-67-3 219778-68-4 219778-70-8 219778-71-9
219778-72-0 219814-52-5 219814-71-8 219814-83-2
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(PCR primer for human gene BRCA1; enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT 9014-24-8, RNA polymerase
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(T3 and T7 RNA polymerase promoter tails in primers for BRCA1 exon amplification; enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

IT 1463-10-1, 5-Methyluridine 2096-10-8, 2,6-Diaminopurine riboside
188254-39-9
RL: BPR (Biological process); BUU (Biological use, unclassified); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(enhanced high d. oligonucleotide **array**-based **sequence** anal. of BRCA1 using modified nucleoside triphosphates)

RE.CNT 31
RE

(1) Chaejoon, C; Nucleic Acids Res 1988, V16, P5115
(2) Chee, M; Science 1996, V274, P610 HCAPLUS
(3) Chollet, A; Nucleic Acids Res 1988, V16, P305 HCAPLUS
(4) Cronin, M; Hum Mutat 1996, V7, P244 HCAPLUS
(5) Fodor, S; Science 1991, V251, P767 HCAPLUS
(6) Froehler, B; Tetrahedron Lett 1992, V33, P5307 HCAPLUS
(7) Guitierrez, A; Biochemistry 1997, V36, P743
(8) Hacia, J; Nature Genet 1996, V14, P441 HCAPLUS
(9) Hacia, J; Nature Genet 1998, V18, P155 HCAPLUS
(10) Hobbs, F; J Org Chem 1989, V54, P3420 HCAPLUS
(11) Hoheisel, J; Nucleic Acids Res 1996, V24, P430 HCAPLUS
(12) Howard, F; Biochemistry 1984, V23, P6723 HCAPLUS
(13) Kozal, M; Nature Med 1996, V2, P753 HCAPLUS
(14) Lockhart, D; Nature Biotech 1996, V14, P1675 HCAPLUS
(15) Ludwig, J; Acta Biochim Biophys Acad Sci Hung 1981, V16, P131 HCAPLUS
(16) McGall, G; Proc Natl Acad Sci USA 1996, V93, P13555 HCAPLUS
(17) Melchior, W; Proc Natl Acad Sci USA 1973, V70, P298 HCAPLUS
(18) Milner, N; Nature Biotech 1997, V15, P537 HCAPLUS
(19) Moffatt, J; J Am Chem Soc 1961, V83, P649
(20) Moriyama, K; Nucleic Acids Res 1998, V26, P2105 HCAPLUS
(21) Piccirilli, J; Nature 1990, V343, P33 HCAPLUS
(22) Ratmeyer, L; Biochemistry 1994, V33, P5298 HCAPLUS
(23) Rees, W; Biochemistry 1993, V32, P137 HCAPLUS
(24) Ricelli, P; Nucleic Acids Res 1993, V21, P3785
(25) Saenger, W; Principles of Nucleic Acid Structure 1984
(26) Shoemaker, D; Nature Genet 1996, V14, P450 HCAPLUS
(27) Sowa, T; Bull Chem Soc Jpn 1975, V48, P2084 HCAPLUS
(28) Tarasow, T; Nature 1997, V389, P54 HCAPLUS
(29) Tor, Y; J Am Chem Soc 1993, V115, P4461 HCAPLUS
(30) Yershov, G; Proc Natl Acad Sci USA 1996, V93, P4913 HCAPLUS
(31) Zimmer, M; Nucleic Acids Res 1984, V12, P2243 HCAPLUS

L108 ANSWER 11 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:283823 HCAPLUS
DN 126:260132
TI Quantification of level of expression of hundreds to millions of genes using **hybridization** to **high density** synthetic oligonucleotide probe **arrays** immobilized on a surface
IN Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
PA Affymax Technologies N.V., Neth.; Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
SO PCT Int. Appl., 126 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
ICS C07H021-04
CC 3-1 (Biochemical Genetics)
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9710365	A1	19970320	WO 1996-US14839	19960913
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6040138	A	20000321	US 1995-529115	19950915
	CA 2232047	AA	19970320	CA 1996-2232047	19960913
	AU 9670734	A1	19970401	AU 1996-70734	19960913
	EP 853679	A1	19980722	EP 1996-931598	19960913
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
	JP 11512293	T2	19991026	JP 1996-512174	19960913
PRAI	US 1995-529115	19950915			
	WO 1996-US14839	19960913			

AB This invention provides methods of monitoring the expression levels of a

multiplicity of genes. The methods involve **hybridizing** a nucleic acid sample to a high d. **array** of oligonucleotide probes where the high d. **array** contains oligonucleotide probes complementary to subsequences of target nucleic acids in the nucleic acid sample. In one embodiment, the method involves providing a pool of target nucleic acids comprising RNA **transcripts** of one or more target genes, or nucleic acids derived from the RNA **transcripts**, **hybridizing** said pool of nucleic acids to an **array** of oligonucleotide probes immobilized on surface, where the **array** comprising more than 100 different oligonucleotides and each different oligonucleotide is localized in a predetd. region of the surface, the d. of the different oligonucleotides is greater than about 60 different oligonucleotides per 1 cm2, and the oligonucleotide probes are complementary to the RNA **transcripts** or nucleic acids derived from the RNA **transcripts**; and quantifying the **hybridized** nucleic acids in the **array**.

ST gene expression quantification **hybridization** oligonucleotide **array**; **high density** oligonucleotide probe **array transcription**

IT Transferrin receptors
.beta.-Actins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(control gene; quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT Cytokines
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene expression; quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(probes; quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT **Computer application**
Gene expression
Immobilization (molecular)
Mouse
Neural network simulation (physicochemical)
Nucleic acid **hybridization**
cDNA library
(quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT DNA
cDNA
mRNA
RL: ANT (Analyte); ANST (Analytical study)
(quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT Genes
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT Microscopy
(scanning confocal fluorescence; quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic oligonucleotide probe **arrays** immobilized on surface)

IT 9001-50-7, Glyceraldehyde phosphate dehydrogenase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(control gene; quantification of level of expression of hundreds to millions of genes using **hybridization** to high d. synthetic

oligonucleotide probe **arrays** immobilized on surface)

L108 ANSWER 12 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:380954 HCAPLUS
DN 125:106773
TI Novel gene **transcripts** preferentially expressed in human muscles revealed by quantitative **hybridization** of a **high density** cDNA **array**
AU Pietu, Genevieve; Alibert, Olivier; Guichard, V. alerie; Lamy, Bernard; Bois, Florence; Leroy, Elisabeth; Mariage-Samson, Regine; Houlgatte, Remi; Soularue, Pascal; Auffray, Charles
CS Genexpress, Centre National Recherche Scientifique, Evry, 91002, Fr.
SO Genome Res. (1996), 6(6), 492-503
CODEN: GEREFS
DT Journal
LA English
CC 3-4 (Biochemical Genetics)
Section cross-reference(s): 13
AB A set of 1091 human skeletal muscle cDNA clone inserts representing more than 800 human gene **transcripts** were spotted as PCR products at high d. on nylon membranes. Replicas of the filters were **hybridized** in stringent conditions with 33P-radiolabeled cDNA probes **transcribed** from skeletal muscle poly(A)+ RNA. **Hybridization** signals were collected on phosphor screens and processed using a software specifically adapted for this application to identify and quantitate each spot. Parameters likely to influence the **hybridization** signal intensity were assessed to eliminate artifacts. Each clone was assigned to one of four intensity classes reflecting the steady-state level of **transcription** of the corresponding gene in skeletal muscle. Differential expression of specific gene **transcripts** was detected using complex cDNA probes derived from nine different tissues, allowing assessment of their tissue specificity. This made is possible to identify 48 novel gene **transcripts** (including 7 homologous or related to known **sequences**) with a muscle-restricted pattern of expression. These results were validated through the anal. of known muscle-specific **transcripts** and by Northern anal. of a subset of the novel gene **transcripts**. All these genes have been registered in the Genexpress Index, such that **sequence**, map, and expression data can be used to decipher their role in the physiol. and pathol. of human muscles.
ST gene cDNA Genexpress index human muscle
IT Muscle
Transcription, genetic
(novel gene **transcripts** preferentially expressed in human muscles revealed by quant. **hybridization** of a high d. cDNA **array**)
IT Gene, animal
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(novel gene **transcripts** preferentially expressed in human muscles revealed by quant. **hybridization** of a high d. cDNA **array**)
IT Deoxyribonucleic acids
RL: BOC (Biological occurrence); PRP (Properties); BIOL (Biological study); OCCU (Occurrence)
(complementary, novel gene **transcripts** preferentially expressed in human muscles revealed by quant. **hybridization** of a high d. cDNA **array**)

L108 ANSWER 13 OF 13 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:74437 HCAPLUS
DN 118:74437
TI **Hybridization** fingerprinting of **high-density** cDNA-library **arrays** with cDNA pools derived from whole tissues
AU Gress, Thomas M.; Hoheisel, Joerg D.; Lennon, Gregory G.; Zehetner,

Guenther; Lehrach, Hans
CS Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SO Mamm. Genome (1992), 3(11), 609-19
CODEN: MAMGEC; ISSN: 0938-8990
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
AB As part of an integrated mapping and **sequencing** anal. of **genomes**, an approach was developed which allows the characterization of large nos. of cDNA library clones with a minimal no. of expts. Three basic elements used in the anal. of cDNA libraries are responsible for the high efficiency of this new approach: (1) high-d. library **arrays** allowing thousands of clones to be screened simultaneously; (2) **hybridization** fingerprinting techniques to identify clones abundantly expressed in specific tissues (by **hybridizations** with labeled tissue cDNA pools) and to avoid the repeated selection of identical clones and of clones contg. noncoding inserts; and (3) a computerized system for the evaluation of **hybridization** data. To demonstrate the feasibility of this approach, high-d. cDNA library **arrays** of human fetal brain and embryonal Drosophila were **hybridized** with radiolabeled cDNA pools derived from whole mouse tissues. Fingerprints of the library **arrays** were generated, localizing clones contg. cDNA **sequences** from mRNAs expressed at middle to high abundance (>0.1-0.15%) in the resp. tissue. Partial **sequencing** data from a no. of clones abundantly expressed in several tissues were generated to demonstrate the value of the approach, esp. for the selection of cDNA clones for the anal. of **genomes** based on expressed **sequence** tagged sites. Data obtained by the technique described will ultimately be correlated with addnl. **transcriptional** and **sequence** information for the same library clones and with **genomic** mapping information in a relational database.
ST cDNA library **hybridization** fingerprinting tissue; clone screening **hybridization** fingerprinting whole tissue
IT Mouse
(cDNA pools derived from whole tissues of, **hybridization** fingerprinting of human fetal brain in Drosophila embryo high-d. cDNA library **arrays** with)
IT Nucleic acid **hybridization**
(fingerprinting, of high d. cDNA library **arrays** with cDNA pools from whole tissue)
IT Drosophila melanogaster
(high-d. cDNA library **arrays** of embryo of, **hybridization** fingerprinting of, with cDNA pools derived from whole mouse tissue)
IT Brain, composition
(human fetal, high-d. cDNA library **arrays** of, **hybridization** fingerprinting of, with cDNA pools from whole mouse tissue)
IT Genetic mapping
(**hybridization** fingerprinting of high-d. cDNA libraries in)
IT Genetic methods
(**hybridization** fingerprinting, of high-d. cDNA library **arrays**, whole tissue-derived cDNA pools for)
IT **Transcription**, genetic
(pattern of, of cDNA clone libraries, **hybridization** fingerprinting with whole tissue-derived cDNA pools for)
IT Deoxyribonucleic acids
RL: BIOL (Biological study)
(complementary, high-d. libraries of, **hybridization** fingerprinting of, cDNA pools from whole tissues in)

=> d all tot

L109 ANSWER 1 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2001:8636 HCAPLUS
TI Analyzing **high-density** oligonucleotide gene expression **array** data
AU Schadt, Eric E.; Li, Cheng; Su, Cheng; Wong, Wing H.
CS Department of Biomathematics, University of California, Los Angeles, CA, 90095, USA
SO J. Cell. Biochem. (2000), 80(2), 192-202
CODEN: JCEBD5; ISSN: 0730-2312
PB Wiley-Liss, Inc.
DT Journal
LA English
CC 3 (Biochemical Genetics)
AB We have developed methods and identified problems assocd. with the anal. of data generated by high-d., oligonuceotide gene expression **arrays**. Our methods are aimed at accounting for many of the sources of variation that make it difficult, at times, to realize consistent results. We present here descriptions of some of these methods and how they impact the anal. of oligonucleotide gene expression **array** data. We will discuss the process of recognizing the "spots" (or features) on the Affymetrix **GeneChip** probe **arrays**, correcting for background and intensity gradients in the resulting images, scaling/normalizing an **array** to allow **array**-to-**array** comparisons, monitoring probe performance with respect to **hybridization** efficiency, and assessing whether a gene is present or differentially expressed. Examples from the analyses of gene expression validation data are presented to contrast the different methods applied to these types of data.
RE.CNT 10
RE
(1) Alon, U; Proc Natl Acad Sci USA 1999, V96, P6745 HCAPLUS
(2) Cox, D; Theoretical statistics 1979
(3) Der, S; Proc Natl Acad Sci USA 1998, V95, P15623 HCAPLUS
(4) Eisen, M; Proc Natl Acad Sci USA 1998, V95, P14863 HCAPLUS
(5) Eisenberg, D; Physical chemistry: with applications to the life sciences 1979
(6) GATC Consortium; GATC Specifications: Software Specifications, http://www.gatconsortium.org/ 1998
(7) Hastie, T; Generalized additive models 1997
(8) Lockhart, D; Nature Biotechnol 1996, V14, P1675 HCAPLUS
(9) Tamayo, P; Proc Natl Acad Sci USA 1999, V96, P2907 HCAPLUS
(10) Wodicka, L; Nature Biotechnol 1997, V5, P1359

L109 ANSWER 2 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:885507 HCAPLUS
TI ComboScreen facilitates the multiplex **hybridization**-based screening of **high-density** clone **arrays**
AU Jamison, D. Curtis; Thomas, James W.; Green, Eric D.
CS Genome Technology Branch, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 20892, USA
SO Bioinformatics (2000), 16(8), 678-684
CODEN: BOINFP; ISSN: 1367-4803
PB Oxford University Press
DT Journal
LA English
CC 3 (Biochemical Genetics)
AB Motivation: The construction of phys. maps based on bacterial clones [e.g. bacterial artificial chromosomes (BACs)] is valuable for a no. of mol. genetics applications, including the high-resoln. mapping of **genomic** regions of interest and the identification of clones suitable for systematic **sequencing**. A common approach for large-scale screening of bacterial clone libraries involves the **hybridization** of high-d. **arrays** of immobilized, lysed colonies with collections of DNA probes. The use of a multiplex **hybridization** screening strategy, whereby pooled probes are analyzed en masse, simplifies the effort by reducing the total no. of

parallel expts. required. However, this approach generates large amts. of **hybridization**-based data that must be carefully analyzed, assimilated, and disambiguated in a careful but efficient manner. Results: To facilitate the screening of high-d. clone **arrays** by a multiplex **hybridization** approach, we have written a program called ComboScreen. This program provides an organizational framework and anal. tools required for the high-throughput **hybridization** screening of clone **arrays** with pools of probes. We have used this program extensively for constructing mouse **sequence**-ready BAC contig maps.

RE.CNT 23

RE

(1) Anon; Genome Res 1998, V8, P1097
(2) Bouffard, G; Genome Res 1997, V7, P673 HCAPLUS
(3) Cai, W; Genomics 1998, V54, P387 HCAPLUS
(4) Collins, F; Science 1998, V282, P682 HCAPLUS
(5) Evans, G; Proc Natl Acad Sci USA 1989, V86, P5030 HCAPLUS
(6) Foote, S; Science 1992, V258, P60 HCAPLUS
(7) Green, E; PCR Methods Appl 1991, V1, P77 HCAPLUS
(8) Green, E; Proc Natl Acad Sci USA 1990, V87, P1213 HCAPLUS
(9) Green, E; Science 1990, V250, P94 HCAPLUS
(10) Hudson, T; Science 1995, V270, P1945 HCAPLUS
(11) Ioannou, P; Nat Genet 1994, V6, P84 HCAPLUS
(12) Lakos, J; Large-Scale C++ Software Design 1996
(13) Magness, C; The SEGMAP Program, htp://www.genome.washington.edu/UWGC/analysistools/segmap.htm 1996
(14) Marra, M; Genome Res 1997, V7, P1072 HCAPLUS
(15) McPherson, J; OvergoMaker 4.0, http://genome.wustl.edu/gsc/overgo/overgo.html 1999
(16) Nagaraja, R; Genome Res 1997, V7, P210 HCAPLUS
(17) Nussbaum, C; Nat Genet 1999, V22, P388
(18) Shizuya, H; Proc Natl Acad Sci USA 1992, V89, P8974
(19) Smart, J; wxWindows Window Toolkit, http://www.wxwindows.org 1999
(20) Stroustrup, B; The C++ Programming Language 1986
(21) Thomas, J; Genome Res 2000, V10, P624 HCAPLUS
(22) Vollrath, D; Genome Analysis: A Laboratory Manual 1999, V4, P187
(23) Wong, G; Proc Natl Acad Sci USA 1997, V94, P5225 HCAPLUS

L109 ANSWER 3 OF 39 HCAPLUS COPYRIGHT 2001 ACS

AN 2000:726029 HCAPLUS

DN 134:68196

TI **High-Density** Fiber-Optic DNA Random Microsphere **Array**

AU Ferguson, Jane A.; Steemers, Frank J.; Walt, David R.

CS Max Tishler Laboratory for Organic Chemistry Department of Chemistry, Tufts University, Medford, MA, 02155, USA

SO Anal. Chem. (2000), 72(22), 5618-5624
CODEN: ANCHAM; ISSN: 0003-2700

PB American Chemical Society

DT Journal

LA English

CC 9-1 (Biochemical Methods)
Section cross-reference(s): 3, 6, 14

AB A high-d. fiber-optic DNA **microarray** sensor was developed to monitor multiple DNA **sequences** in parallel. **Microarrays** were prepd. by randomly distributing DNA probe-functionalized 3.1-.mu.m-diam. microspheres in an **array** of wells etched in a 500-.mu.m-diam. optical imaging fiber. Registration of the microspheres was performed using an optical encoding scheme and a custom-built imaging system. **Hybridization** was visualized using fluorescent-labeled DNA targets with a detection limit of 10 fM. **Hybridization** times of seconds are required for nanomolar target concns., and anal. is performed in minutes.

ST DNA fiber optic microsphere **array** fluorescein cystic fibrosis

IT DNA
RL: ANT (Analyte); ANST (Analytical study)

(fluorescein labeled; high-d. fiber-optic DNA random microsphere **array**)
IT Microspheres
(fluorescent; high-d. fiber-optic DNA random microsphere **array**)
IT Biosensors
Cystic fibrosis
Diagnosis
Immobilization, biochemical
Nucleic acid **hybridization**
(high-d. fiber-optic DNA random microsphere **array**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(high-d. fiber-optic DNA random microsphere **array**)
IT 2321-07-5, Fluorescein
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(high-d. fiber-optic DNA random microsphere **array**)
IT 200737-72-0 314777-87-2 314777-88-3 314777-89-4 314777-90-7
314777-91-8 314777-92-9 314777-93-0 314777-94-1 314777-95-2
314777-96-3 314777-97-4 315251-67-3 315251-68-4 315251-69-5
315251-70-8 315251-71-9 315251-72-0 315251-73-1 315251-74-2
315251-75-3 315251-76-4 315251-77-5 315251-78-6 315251-79-7
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(high-d. fiber-optic DNA random microsphere **array**)
RE.CNT 33
RE
(1) Baba, Y; J Chromatogr, B: Biomed Appl 1996, V687, P271 HCAPLUS
(2) Bangs, L; Uniform Latex Particles 1984
(3) Bronk, K; Anal Chem 1995, V67, P2750 HCAPLUS
(4) Brown, P; Nat Genet 1999, V21(1 Suppl), P33 MEDLINE
(5) Chee, M; Science 1996, V274, P610 HCAPLUS
(6) Cronin, M; Hum Mutat 1996, V7, P244 HCAPLUS
(7) Czarnik, A; Curr Opin Chem Biol 1997, V1, P60 HCAPLUS
(8) Derisi, J; Nat Genet 1996, V14, P457 HCAPLUS
(9) Desaizieu, A; Nat Biotechol 1998, V16, P45 HCAPLUS
(10) Egner, B; Chem Commun 1997, V8, P735
(11) Ferguson, J; Nat Biotechnol 1996, V14, P1681 HCAPLUS
(12) Fulton, R; Clin Chem 1997, V43, P1749 HCAPLUS
(13) Hacia, J; Nat Genet 1996, V14, P441 HCAPLUS
(14) Hakala, H; Bioconjugate Chem 1997, V8, P232 HCAPLUS
(15) Hakala, H; Bioconjugate Chem 1997, V8, P378 HCAPLUS
(16) Haugland, R; Handbook of Fluorescent Probes and Research Chemicals 1996
(17) Healey, B; Anal Biochem 1997, V251, P270 HCAPLUS
(18) Lander, E; Science 1996, V274, P536 HCAPLUS
(19) Lockhart, D; Nature 2000, V405, P827 HCAPLUS
(20) McGall, G; Proc Natl Acad Sci U S A 1996, V93, P13555 HCAPLUS
(21) Michael, K; Anal Chem 1998, V70, P1242 HCAPLUS
(22) Needels, M; Proc Natl Acad Sci U S A 1993, V90, P10700 HCAPLUS
(23) Pantano, P; Anal Chem 1995, V67, P481A HCAPLUS
(24) Pantano, P; Chem Mater 1996, V8, P2832 HCAPLUS
(25) Schena, M; Proc Natl Acad Sci U S A 1996, V93, P10614 HCAPLUS
(26) Shalon, D; Genome Res 1996, V6, P639 HCAPLUS
(27) Shuber, A; Hum Mol Genet 1997, V6, P337 HCAPLUS
(28) Storhoff, J; J Am Chem Soc 1998, V120, P1959 HCAPLUS
(29) van Ness, J; Nucleic Acids Res 1991, V19, P3345 HCAPLUS
(30) Wallraff, G; ChemTech 1997, V27, P22 HCAPLUS
(31) Walt, D; Science 2000, V287, P451 HCAPLUS
(32) Walt, D; Trends Anal Chem 1994, V13, P425 HCAPLUS
(33) Wang, D; Science 1998, V280, P1077 HCAPLUS

L109 ANSWER 4 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:423131 HCAPLUS
DN 133:306050

TI Parallel genotyping of human SNPs using generic **high-density** oligonucleotide tag **arrays**
AU Fan, Jian-Bing; Chen, Xiaoqiong; Halushka, Marc K.; Berno, Anthony; Huang, Xiaohua; Ryder, Thomas; Lipshutz, Robert J.; Lockhart, David J.; Chakravarti, Aravinda
CS Affymetrix, Inc., CA, 95051, USA
SO Genome Res. (2000), 10(6), 853-860
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 13
AB Large scale human genetic studies require technologies for generating millions of genotypes with relative ease but also at a reasonable cost and with high accuracy. We describe a highly parallel method for genotyping single nucleotide polymorphisms (SNPs), using generic high-d. oligonucleotide **arrays** that contain thousands of preselected 20-mer oligonucleotide tags. First, marker-specific primers are used in PCR amplifications of **genomic** regions contg. SNPs. Second, the amplification products are used as templates in single base extension (SBE) reactions using chimeric primers with 3' complementarity to the specific SNP loci and 5' complementarity to specific probes, or tags, synthesized on the **array**. The SBE primers, terminating one base before the polymorphic site, are extended in the presence of labeled dideoxy NTPs, using a different label for each of the two SNP alleles, and **hybridized** to the tag **array**. Third, genotypes are deduced from the fluorescence intensity ratio of the two colors. This approach takes advantage of multiplexed sample prepn., **hybridization**, and anal. at each stage. We illustrate and test this method by genotyping 44 individuals for 142 human SNPs identified previously in 62 candidate hypertension genes. Because the **hybridization** results are quant., this method can also be used for allele-frequency estn. in pooled DNA samples.
ST genotyping single nucleotide polymorphism TAG SBE **hybridization** tag **array**
IT Genotyping (method)
(TAG-SBE (single-base extension); parallel genotyping of human SNPs using generic high-d. oligonucleotide tag **arrays**)
IT Fluorometry
Nucleic acid **hybridization**
PCR (polymerase chain reaction)
(parallel genotyping of human SNPs using generic high-d. oligonucleotide tag **arrays**)
IT DNA
RL: ANT (Analyte); ANST (Analytical study)
(parallel genotyping of human SNPs using generic high-d. oligonucleotide tag **arrays**)
IT Genetic polymorphism
(single nucleotide; parallel genotyping of human SNPs using generic high-d. oligonucleotide tag **arrays**)
IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(tag **arrays**; parallel genotyping of human SNPs using generic high-d. oligonucleotide tag **arrays**)
RE.CNT 32
RE
(1) Cargill, M; Nature Genet 1999, V22, P231 HCAPLUS
(2) Chakravarti, A; Nature Genet 1999, V21, P56 HCAPLUS
(3) Chee, M; Science 1996, V274, P610 HCAPLUS
(4) Chen, X; Genome Res 1998, V8, P549 HCAPLUS
(5) Chen, X; Nucleic Acids Res 1997, V25, P347 HCAPLUS
(6) Chen, X; Proc Natl Acad Sci 1997, V94, P10756 HCAPLUS
(7) Collins, F; Science 1997, V278, P1580 HCAPLUS
(8) Collins, F; Science 1998, V282, P682 HCAPLUS
(9) Delahunty, C; Am J Hum Genet 1996, V58, P1239 HCAPLUS

(10) Giaever, G; Nature Genet 1999, V21, P278 HCAPLUS
(11) Hacia, J; Nucleic Acids Res 1998, V26, P3865 HCAPLUS
(12) Halushka, M; Nature Genet 1999, V22, P239 HCAPLUS
(13) Head, S; Nucleic Acids Res 1997, V25, P5065 HCAPLUS
(14) Kuppuswamy, M; Proc Natl Acad Sci 1991, V88, P1143 HCAPLUS
(15) Lipshutz, R; Nature Genet 1999, V21, P20 HCAPLUS
(16) Lo, Y; Nucleic Acids Res 1991, V19, P3561 HCAPLUS
(17) Lyamichev, V; Nature Biotech 1999, V17, P292 HCAPLUS
(18) Newton, C; Nucleic Acids Res 1989, V17, P2503 HCAPLUS
(19) Nikiforov, T; Nucleic Acids Res 1994, V22, P4167 HCAPLUS
(20) Pastinen, T; Genome Res 1997, V7, P606 HCAPLUS
(21) Pastinen, T; Hum Mol Genet 1998, V7, P1453 HCAPLUS
(22) Risch, N; Science 1996, V273, P1516 HCAPLUS
(23) Shaw, S; Genome Res 1998, V8, P111 HCAPLUS
(24) Shoemaker, D; Nature Genet 1996, V14, P450 HCAPLUS
(25) Syvanen, A; Am J Hum Genet 1993, V52, P46 HCAPLUS
(26) Syvanen, A; Genomics 1990, V8, P684 HCAPLUS
(27) Syvanen, A; Methods Mol Biol 1998, V98, P291 MEDLINE
(28) Tobe, V; Nucleic Acids Res 1996, V24, P3728 HCAPLUS
(29) Wang, D; Science 1998, V280, P1077 HCAPLUS
(30) Winzeler, E; Science 1998, V281, P1194 HCAPLUS
(31) Winzeler, E; Science 1999, V285, P901 HCAPLUS
(32) Wodicka, L; Nat Biotechnology 1997, V15, P1359 HCAPLUS

L109 ANSWER 5 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:333909 HCAPLUS
DN 134:1098
TI **High-density** oligonucleotide probe **arrays**
AU McGall, Glenn H.; Fidenza, Jacqueline A.
CS Affymetrix, Inc., Santa Clara, CA, USA
SO Proc. SPIE-Int. Soc. Opt. Eng. (2000), 3926(Advances in Nucleic Acid and Protein Analyses, Manipulation, and Sequencing), 106-110
CODEN: PSISDG; ISSN: 0277-786X
PB SPIE-The International Society for Optical Engineering
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 6, 9
AB High-d. DNA probe **arrays** offer a massively parallel approach to nucleic acid **sequence** anal. that will have a major impact on gene-based biomedical research and clin. diagnostics. Light-directed synthesis has enabled the large- scale manuf. of **arrays** contg. hundreds of thousands of oligonucleotide probe **sequences** on a glass "chip" about 1.6 cm2 in size. This method is used to produce high-d. **GeneChipTM** probe **arrays**, which are now finding widespread use in the detection and anal. of mutations and polymorphisms ("genotyping"), and in a wide range of gene expression studies. This paper will discuss methods for high-resoln. photolithog. **array** fabrication which integrate solid-phase oligonucleotide synthesis, photochem. removable protecting groups, and lithog. techniques adapted from the microelectronics industry.
ST nucleic acid probe **hybridization GeneChip** app DNA
IT Apparatus
(**GeneChip**; high-d. oligonucleotide probe **arrays**)
IT DNA **sequences**
Nucleic acid **hybridization**
RNA **sequences**
(high-d. oligonucleotide probe **arrays**)
IT DNA
RNA
RL: ANT (Analyte); ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)
(high-d. oligonucleotide probe **arrays**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study);

PROC (Process); USES (Uses)
(high-d. oligonucleotide probe **arrays**)
RE.CNT 34
RE
(1) Anon; Nature Genetics 1999, V21(1/Supplement), P1
(2) Barone, A; Nucleic Acids Res 1984, V12, P4051 HCAPLUS
(3) Beecher, J; Preprints Amer Chem Soc Div Polym Mater Sci Eng 1997, V76, P597 HCAPLUS
(4) Broude, N; Proc Natl Acad Sci USA 1994, V91, P3072 HCAPLUS
(5) Chee, M; Science 1996, V274, P610 HCAPLUS
(6) Cheong, C; Nucleic Acids Res 1988, V16, P5115 HCAPLUS
(7) Chollet, A; Chem Scripta 1985, V26, P37
(8) Chollet, A; Chem Scripta 1994, V26, P37
(9) Fidanza, J; to be published in Nucleosides and Nucleotides 1999, V10
(10) Fodor, S; Science 1991, V251, P767 HCAPLUS
(11) Gaffney, B; Tetrahedron 1984, V40, P3 HCAPLUS
(12) Giegrich, H; Nucleosides and Nucleotides 1998, V17, P1987 HCAPLUS
(13) Gryaznov, S; Tetrahedron Lett 1994, V35, P2489 HCAPLUS
(14) Gunderson, K; Genomics Res 1998, V8, P1142 HCAPLUS
(15) Hasan, A; Tetrahedron 1997, V53, P4247 HCAPLUS
(16) Hoheisel, J; FEBS Letters 1990, V274, P103 HCAPLUS
(17) Howard, F; Biochemistry 1984, V23, P6723 HCAPLUS
(18) Inoue, H; Nucleic Acids Res 1987, V15, P6131 HCAPLUS
(19) Kozal, M; Nature Medicine 1996, V7, P753
(20) Lipshutz, R; Nature Genetics 1999, V21(1/Supplement), P20
(21) Lockhart, D; Nature Biotechnology 1996, V14, P1675 HCAPLUS
(22) Majlessi, M; Nucleic Acids Res 1998, V26, P2224 HCAPLUS
(23) Maskos, U; Nucleic Acids Res 1993, V21, P4663 HCAPLUS
(24) McGall, G; Biochip Arrays and Integrated Devices for Clinical Diagnostics 1997, P2.1
(25) McGall, G; J Amer Chem Soc 1997, V119, P5081 HCAPLUS
(26) McGall, G; Proc Natl Acad Sci USA 1996, V93, P13555 HCAPLUS
(27) Pease, A; Proc Natl Acad Sci USA 1994, V91, P5022 HCAPLUS
(28) Pirrung, M; Bioorganic & Medicinal Chemistry Letters 1994, V4, P1345 HCAPLUS
(29) Pirrung, M; J Org Chem 1995, V60, P1116 HCAPLUS
(30) Pirrung, M; J Org Chem 1995, V60, P6270 HCAPLUS
(31) Pirrung, M; J Org Chem 1998, V63, P241 HCAPLUS
(32) Prosnyak, M; Genomics 1994, V21, P490 HCAPLUS
(33) van Boom, J; Oligonucleotide Synthesis: A practical Approach 1984, P153
(34) Wallraff, G; Chemtech 1997, February, P22

L109 ANSWER 6 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:98926 HCAPLUS
DN 132:133202
TI A rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction
IN Mirzabekov, Andrei Darievich; Yershov, Gennadiy Moiseyevich; Guschin, Dmitry Yuryevich; Gemmell, Margaret Anne; Shick, Valentine V.; Proudnikov, Dmitri Y.; Timofeev, Edward N.
PA The University of Chicago, USA
SO PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM G01N033-553
ICS G01N033-544; B05D001-00
CC 3-1 (Biochemical Genetics)
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000007022	A1	20000210	WO 1999-US17586	19990802

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK,

MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD,
RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK,
ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG,
CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9956701 A1 20000221 AU 1999-56701 19990802
PRAI US 1998-127313 19980731
WO 1999-US17586 19990802

AB A method for detg. the existence of duplexes of oligonucleotide complementary mols. is provided whereby a plurality of immobilized oligonucleotide mols., each of a specific length and each having a specific base **sequence**, is contacted with complementary, single-stranded oligonucleotide mols. to form a duplex so as to facilitate intercalation of a fluorescent dye between the base planes of the duplex. The invention also provides for a method for constructing oligonucleotide matrixes comprising confining light-sensitive fluid to a surface, exposing said light-sensitive fluid to a light pattern so as to cause the fluid exposed to the light to polymerize into discrete units and adhere to the surface; and contacting each of the units with a set of different oligonucleotide mols. so as to allow the mols. to disperse into the units. The method can produce a polyacrylamide matrix having thousands of individual and well-defined holding cells, the advantage of which is the rendering of high nos. of precise cell geometries and at **high densities**. A feature of the invention is the use of mask-controlled photopolymn. processes. The **array** manufg. method incorporated a modified methylene blue- or non-methylene blue-induced photopolymn. procedure whereby a polyacrylamide soln. is prepd. and then configured into desired shapes and sizes for subsequence polymn.

ST oligonucleotide duplex detection immobilization photopolymn; **sequencing hybridization** duplex detection immobilization

IT DNA **sequence** analysis
Nucleic acid **hybridization**
(SHOM (**sequencing** by **hybridization** on oligonucleotide matrixes); rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(matrixes; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT Polymerization
(photopolymn.; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT Immobilization, biochemical
UV radiation
(rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT DNA
RL: ANT (Analyte); ANST (Analytical study)
(rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT Oligodeoxyribonucleotides
Oligonucleotides
RL: ARG (Analytical reagent use); DEV (Device component use); PEP (Physical, engineering or chemical process); ANST (Analytical study); PROC (Process); USES (Uses)
(rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)

IT 61-73-4, Methylene blue
RL: BUU (Biological use, unclassified); RCT (Reactant); BIOL (Biological study); USES (Uses)
(light-sensitive fluid contg. acrylamide and TEMED and; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)
IT 79-06-1, Acrylamide, biological studies
RL: BUU (Biological use, unclassified); RCT (Reactant); BIOL (Biological study); USES (Uses)
(light-sensitive fluid contg. methylene blue and TEMED and; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)
IT 110-18-9, TEMED
RL: BUU (Biological use, unclassified); RCT (Reactant); BIOL (Biological study); USES (Uses)
(light-sensitive fluid contg. methylene blue and acrylamide and; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)
IT 67-64-1, Acetone, biological studies 101-29-1, 3,5-Diiodo-4-pyridone-N-acetic acid 110-26-9, Bisacrylamide 2638-94-0, 4,4'-Azobis(4-cyanovaleric acid) 24650-42-8, 2,2-Dimethoxy-2-phenylacetophenone 50438-75-0, 2-(4-Dimethylaminophenyl)ethanol 57951-36-7, Dimethylaminopyridine
RL: BUU (Biological use, unclassified); RCT (Reactant); BIOL (Biological study); USES (Uses)
(photopolymn. agent; rapid method to detect duplex formation in **sequencing** by **hybridization** methods and a method for constructing containment structures for reagent interaction)
RE.CNT 4
RE
(1) Guschin, D; Analytical Biochemistry 1997, V250, P203 HCAPLUS
(2) Lockhart; US 5556752 A 1996 HCAPLUS
(3) Timofeev, E; Nucleic Acids Research 1996, V24(16), P3142 HCAPLUS
(4) Vasiliskov, A; BioTechniques 1999, V27(3), P592 HCAPLUS

L109 ANSWER 7 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:44881 HCAPLUS
DN 133:69446
TI Light-directed synthesis of **high-density** oligonucleotide probe **arrays** for nucleic acid **sequence** analysis
AU McGall, Glenn H.; Barone, A. Dale; Beecher, Jody E.; Diggelman, Martin; Fodor, Steven P. A.; Goldberg, Martin J.; Ngo, Nam; Rava, Richard P.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Innovation Perspect. Solid Phase Synth. Comb. Libr., Collect. Pap., Int. Symp., 5th (1999), Meeting Date 1997, 97-100. Editor(s): Epton, Roger. Publisher: Mayflower Scientific Ltd., Kingswinford, UK.
CODEN: 68OEAA
DT Conference; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 34
AB A review with 9 refs. The high-d. polynucleotide probe **array** has emerged as a powerful new tool for accessing genetic information on a large scale using **hybridization**. In the Affymetrix **GeneChip**.RTM. system, analyte DNA or RNA "target" **sequences** are fragmented, labeled with a fluorescent tag, and allowed to **hybridize** with an **array** under controlled conditions. High-resoln. images of surface fluorescence indicate which probes in the **array** correspond to complementary **sequences** in the sample. **Arrays** are currently available which can analyze hundreds of kilobases of **sequence** simultaneously for applications including gene expression monitoring,

genotyping, or resequencing. In developing this technol., one of the primary challenges has been to implement methods of fabricating **arrays** with a very high d. of encoded **sequence** information, for manufg. on a scale. This review summarizes recent developments in the chem. of **array** fabrication using photolithog. techniques adapted from the microelectronics industry.
ST review oligonucleotide probe **array** synthesis photolithog; **hybridization** oligonucleotide probe **array** synthesis review
IT Nucleic acid **hybridization**
Photolithography
(light-directed synthesis of high-d. oligonucleotide probe **arrays** for nucleic acid **sequence** anal.)
IT Oligonucleotides
RL: ARG (Analytical reagent use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(light-directed synthesis of high-d. oligonucleotide probe **arrays** for nucleic acid **sequence** anal.)
IT Probes (nucleic acid)
RL: SPN (Synthetic preparation); PREP (Preparation)
(light-directed synthesis of high-d. oligonucleotide probe **arrays** for nucleic acid **sequence** anal.)
RE.CNT 9
RE
(1) Anderson, R; Top Curr Chem 1998, V194, P117 HCAPLUS
(2) Beecher, J; Preprints Amer Chem Soc Div Polym Mater Sci Eng 1997, V76, P597 HCAPLUS
(3) Chee, M; Science 1996, V274, P610 HCAPLUS
(4) Fodor, S; Science 1991, V251, P767 HCAPLUS
(5) Lockhart, D; Nat Biotechnol 1997, V14, P1675
(6) McGall, G; J Amer Chem Soc 1997, V119, P5081 HCAPLUS
(7) McGall, G; Proc Natl Acad Sci USA 1996, V93, P13555 HCAPLUS
(8) Pease, A; Proc Natl Acad Sci USA 1994, V91, P5022 HCAPLUS
(9) Wallraff, G; Chemtech 1997, P22 HCAPLUS

L109 ANSWER 8 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:819105 HCAPLUS
DN 132:60096
TI Parallel screening of allelic variation by **hybridization** with **high-density arrays**
IN Winzeler, Elizabeth; Richards, Dan; Davis, Ronald
PA Board of Trustees of the Leland S. Stanford Junior University, USA
SO Eur. Pat. Appl., 25 pp.
CODEN: EPXXDW
DT Patent
LA English
IC ICM C12Q001-68
CC 3-1 (Biochemical Genetics)
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 967291	A1	19991229	EP 1999-250176	19990604
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2000041687	A2	20000215	JP 1999-160264	19990607

PRAI US 1998-93947 19980608
AB Parallel **hybridization** anal. is used to detect and analyze allelic variation between 2 closely related **genomic** nucleic acid samples. Nucleic acid samples from both sources are cleaved to generate short fragments. The fragments are end-labeled, and then **hybridized** to a high-d. oligonucleotide **array**. **Hybridization** patterns for the 2 samples are detected, normalized and compared. Those positions on the **array** that correspond to **sequences** with allelic variation between the 2 samples show decreased **hybridization** efficiency for one of the samples relative to the other. A map of allelic variation can be generated with

this information, and used for genetic linkage anal., detn. of chromosomal regions having low diversity or high diversity, forensic studies, etc.
ST allele variation parallel **hybridization** screening
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(high-d. **array**; parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
IT Avidins
Phycoerythrins
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(label; parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
IT Nucleic acid **hybridization**
(parallel **hybridization** anal.; parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
IT Alleles
Genetic polymorphism
Saccharomyces cerevisiae
(parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
IT 58-85-5
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(label; parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
IT 252967-28-5, 1: PN: EP967291 SEQID: 1 unclaimed DNA 252967-29-6, 2: PN: EP967291 SEQID: 2 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide **sequence**; parallel screening of allelic variation by **hybridization** with high-d. **arrays**)
RE.CNT 7
RE
(1) Beattie, K; WO 9722720 A 1997 HCAPLUS
(2) Chee, M; Science 1996, V274, P610 HCAPLUS
(3) Gingeras, T; WO 9729212 A 1997 HCAPLUS
(4) Lashkari, D; Proceedings of the National Academy of Sciences of the United States of America 1997, V94, P13057 HCAPLUS
(5) Wang, D; Science 1998, V280, P1077 HCAPLUS
(6) Winzeler, E; Science 1998, V281(5380), P1194 HCAPLUS
(7) Wodicka; Nature Biotechnology 1997, V15(15), P1359

L109 ANSWER 9 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:514896 HCAPLUS
DN 131:267673
TI **High-density** nucleoside analog probe **arrays** for enhanced **hybridization**
AU Fidanza, Jacqueline A.; McGall, Glenn H.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Nucleosides Nucleotides (1999), 18(6 & 7), 1293-1295
CODEN: NUNUD5; ISSN: 0732-8311
PB Marcel Dekker, Inc.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB DNA probe **arrays** were synthesized with analogs of 2,6-diaminopurine and 2'-O-methyl-thymidine in place of A and T. AT-rich **GeneChip** test **arrays** contg. 14-mer or 20-mer analog probes improved **hybridization** to fluorescently-labeled RNA **sequences** under stringent conditions.
ST nucleoside **high density** analog probe **array** enhanced **hybridization**
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(14-mer or 20-mer, with 2,6-diaminopurine and 2'-O-methyl-thymidine in

place of A and T; high-d. nucleoside analog probe **arrays** for enhanced **hybridization**)
IT Nucleosides, biological studies
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(2'-O-Me; high-d. nucleoside analog probe **arrays** for enhanced **hybridization**)
IT Nucleic acid **hybridization**
(DNA-DNA; high-d. nucleoside analog probe **arrays** for enhanced **hybridization**)
IT 55486-09-4 80791-87-3
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(2,6-diaminopurine and 2'-O-methyl-thymidine in place of A and T; high-d. nucleoside analog probe **arrays** for enhanced **hybridization**)
RE.CNT 8
RE
(1) Chronin, M; Hum Mutat 1996, V7, P244
(2) Gao, H; J Org Chem 1992, V57, P6954 HCAPLUS
(3) Gryaznov, D; Tetrahedron Lett 1994, V35, P2489
(4) Inoue, H; Nucleic Acids Res 1987, V15, P6131 HCAPLUS
(5) Kozal, M; Nat Med 1996, V2, P753 HCAPLUS
(6) Lipshutz, R; Biotechniques 1995, V19, P442 HCAPLUS
(7) McGall, G; J Am Chem Soc 1997, V119, P5081 HCAPLUS
(8) Pease, A; Proc Natl Acad Sci USA 1994, V91, P5022 HCAPLUS

L109 ANSWER 10 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:496131 HCAPLUS
DN 131:282038
TI **High density** oligonucleotide and DNA probe **arrays** for the analysis of target DNA
AU Thompson, Michael; Michelle Furtado, L.
CS Department of Chemistry, University of Toronto, Toronto, ON, M5S 3H6, Can.
SO Analyst (Cambridge, U. K.) (1999), 124(8), 1133-1136
CODEN: ANALAO; ISSN: 0003-2654
PB Royal Society of Chemistry
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 6, 9
AB A review, with 19 refs. The acquisition of **sequence**, expression and other information concerning genetic material constitutes a crucial component of the modern revolution in mol. biol. One important advance in this area is the development of high d. oligonucleotide/DNA **microarrays** which allows the rapid **sequence** anal. of **genomic** target samples in addn. to diagnostic possibilities with respect to genetic and infectious disease. In the present article we review protocols for the design of such **microarrays** and their principles of operation. Together with a look at some recent applications we include brief remarks as to the possibilities for the future.
ST review DNA oligonucleotide probe **array hybridization**
IT DNA **sequences**
Diagnosis
Nucleic acid **hybridization**
(high d. oligonucleotide and DNA probe **arrays** for the anal. of target DNA)
IT DNA
Oligonucleotides
RNA
RL: ANT (Analyte); ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)
(high d. oligonucleotide and DNA probe **arrays** for the anal. of target DNA)
IT Probes (nucleic acid)

RL: ARU (Analytical role, unclassified); BPR (Biological process); ANST (Analytical study); BIOL (Biological study); PROC (Process)
(high d. oligonucleotide and DNA probe **arrays** for the anal. of target DNA)
IT Apparatus
(**microarray**; high d. oligonucleotide and DNA probe **arrays** for the anal. of target DNA)
RE.CNT 19
RE
(1) Anon; http:/www.affymetrix.com
(2) Anon; www.synteni.org
(3) Caviani, A; Proc Natl Acad Sci 1994, V81, P5022
(4) Chee, M; Science 1996, V274, P610 HCAPLUS
(5) DeRisi, J; Science 1997, V278, P680 HCAPLUS
(6) Drmanac, R; Science 1993, V260, P1649 HCAPLUS
(7) Fodor, S; Science 1991, V251, P767 HCAPLUS
(8) Hacia, J; Nature Genetics 1996, V14, P441 HCAPLUS
(9) Hacia, J; Nature Genetics 1998, V18, P155 HCAPLUS
(10) Hacia, J; Nucl Acid Res 1998, V26, P3865 HCAPLUS
(11) Hawkins, J; Drug and Market Development 1997, 938
(12) Kreiner, T; Am Lab 1996, P39 HCAPLUS
(13) Lipshutz, R; Biotech 1995, V19, P442 HCAPLUS
(14) Maxam, A; Proc Natl Acad Sci 1977, V74, P560 HCAPLUS
(15) Mazzola, L; Biophys J 1985, V73, P1653
(16) Sanger, F; Proc Natl Acad Sci 1977, V74, P5463 HCAPLUS
(17) Schena, M; Science 1995, V270, P467 HCAPLUS
(18) Yang, M; Anal Chim Acta 1997, V346, P259 HCAPLUS
(19) Yershof, G; Proc Natl Acad Sci 1996, V93, P4913

L109 ANSWER 11 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:461861 HCAPLUS
DN 131:209694
TI Chemiluminescent detection of sequential DNA **hybridizations** to **high-density**, filter-**arrayed** cDNA libraries: a subtraction method for novel gene discovery
AU Guiliano, D.; Ganatra, M.; Ware, J.; Parrot, J.; Daub, J.; Moran, L.; Brennecke, H.; Foster, J. M.; Supali, T.; Blaxter, M.; Scott, A. L.; Williams, S. A.; Slatko, B. E.
CS University of Edinburgh, Edinburgh, UK
SO BioTechniques (1999), 27(1), 146-150, 152
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB A chemiluminescent approach for sequential DNA **hybridizations** to high-d. filter **arrays** of cDNAs, using a biotin-based random priming method followed by a streptavidin/alk. phosphatase/CDP-Star detection protocol, is presented. The method has been applied to the Brugia malayi **genome** project, wherein cDNA libraries, cosmid and bacterial artificial chromosome (BAC) libraries have been gridded at high d. onto nylon filters for subsequent anal. by **hybridization**. Individual probes and pools of rRNA probes, ribosomal protein probes and expressed **sequence** tag probes show correct specificity and high signal-to-noise ratios even after ten rounds of **hybridization**, detection, stripping of the probes from the membranes and rehybridization with addnl. probe sets. This approach provides a subtraction method that leads to a redn. in redundant DNA **sequencing**, thus increasing the rate of novel gene discovery. The method is also applicable for detecting target **sequences**, which are present in one or only a few copies per cell; it has proven useful for phys. mapping of BAC and cosmid high d. filter **arrays**, wherein multiple probes have been **hybridized** at one time (multiplexed) and subsequently "deplexed" into individual components for specific probe localizations.
ST chemiluminescent detection sequential DNA **hybridization**

subtractive cDNA gene discovery
IT Nucleic acid **hybridization**
(DNA-DNA; chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries: a subtraction method for novel gene discovery)
IT Chromosome
(bacterial artificial, phys. mapping of; chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries, a subtraction method for novel gene discovery)
IT cDNA library
(chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries, a subtraction method for novel gene discovery)
IT Luminescence, chemiluminescence
(chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries: a subtraction method for novel gene discovery)
IT Gene
RL: ANT (Analyte); BSU (Biological study, unclassified); ANST (Analytical study); BIOL (Biological study)
(discovery; chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries, a subtraction method for novel gene discovery)
IT DNA **sequence** analysis
(leads to redn. in redundant; chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries, a subtraction method for novel gene discovery)
IT Molecular cloning
(subtractive; chemiluminescent detection of sequential DNA **hybridizations** to high-d., filter-**arrayed** cDNA libraries, a subtraction method for novel gene discovery)
RE.CNT 14
RE
(1) Becker, P; Proc Natl Acad Sci USA 1991, V88, P4109 HCAPLUS
(2) Becker-Andre, M; Nucleic Acids Res 1989, V17, P9437 HCAPLUS
(3) Celi, F; Nucleic Acids Res 1993, V21, P1047 HCAPLUS
(4) Chomczynski, P; Anal Biochem 1987, V162, P156 HCAPLUS
(5) Ercolani, L; J Biol Chem 1988, V263, P15335 HCAPLUS
(6) Gilliland, G; Proc Natl Acad Sci USA 1990, V87, P2725 HCAPLUS
(7) Iyer, V; Proc Natl Acad Sci USA 1996, V93, P5208 HCAPLUS
(8) Lyons, J; Int J Cancer 1989, V43, P119 HCAPLUS
(9) Piechaczyk, M; Nucleic Acids Res 1984, V12, P6951 HCAPLUS
(10) Raeymaekers, L; Anal Biochem 1993, V214, P582 HCAPLUS
(11) Saiki, R; Science 1985, V230, P1350 HCAPLUS
(12) Stevenson, G; Biosci Rep 1985, V5, P1071 HCAPLUS
(13) Zhang, L; Science 1997, V276, P1268 HCAPLUS
(14) Zimmerman, K; BioTechniques 1996, V21, P268

L109 ANSWER 12 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:188641 HCAPLUS
DN 131:28417
TI High-throughput polymorphism screening and genotyping with **high-density** oligonucleotide **arrays**
AU Sapolsky, Ronald J.; Hsie, Linda; Berno, Anthony; Ghandour, Ghassan; Mittmann, Michael; Fan, Jian-Bing
CS Stanford DNA Sequencing and Technology Center, Stanford University, Stanford, CA, 94305, USA
SO Genet. Anal.: Biomol. Eng. (1999), 14(5-6), 187-192
CODEN: GEANF4; ISSN: 1050-3862
PB Elsevier Science B.V.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9, 13
AB A highly reliable and efficient technol. has been developed for

high-throughput DNA polymorphism screening and large-scale genotyping. Photolithog. synthesis has been used to generate miniaturized, high-d. oligonucleotide **arrays**. Dedicated instrumentation and software have been developed for **array hybridization**, fluorescent detection, and data acquisition and anal. Specific oligonucleotide probe **arrays** have been designed to rapidly screen human STSs, known genes and full-length cDNAs. This has led to the identification of several thousand biallelic single-nucleotide polymorphisms (SNPs). Meanwhile, a rapid and robust method has been developed for genotyping these SNPs using oligonucleotide **arrays** . Each allele of an SNP marker is represented on the **array** by a set of perfect match and mismatch probes. Prototype genotyping chips have been produced to detect 400, 600 and 3000 of these SNPs. Based on the preliminary results, using oligonucleotide **arrays** to genotype several thousand polymorphic loci simultaneously appears feasible.

ST polynucleotide high throughput screening genotyping oligonucleotide **array**

IT Probes (nucleic acid)
RL: BAC (Biological activity or effector, except adverse); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(each allele of an SNP marker is represented on the **array** by a set of perfect match and mismatch probes; high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

IT Genotyping (method)
(high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

IT **Computer program**
(instrumentation and software have been developed; high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

IT Oligonucleotides
RL: BAC (Biological activity or effector, except adverse); BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(photolithog. synthesis used to generate miniaturized, high-d. oligonucleotide **arrays**; high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

IT Genetic polymorphism
(single nucleotide; high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

IT Gene, animal
STS (**sequence**-tagged site)
cDNA
RL: ANT (Analyte); PRP (Properties); ANST (Analytical study)
(specific oligonucleotide probe **arrays** have been designed to rapidly screen human STSs, known genes and full-length cDNAs; high-throughput polymorphism screening and genotyping with high-d. oligonucleotide **arrays**)

RE.CNT 27

RE

(1) Chee, M; Science 1996, V274, P610 HCAPLUS
(2) Cho, R; Molec Cell 1998, V2, P65 HCAPLUS
(3) Cho, R; Proc Nat Acad Sci USA 1998, V95, P3752 HCAPLUS
(4) Collins, F; Science 1997, V278, P1580 HCAPLUS
(5) Cronin, M; Hum Mutat 1996, V7, P244 HCAPLUS
(6) de Saizieu, A; Nat Biotechnol 1998, V16, P45 HCAPLUS
(7) Dib, C; Nature 1996, V380, P152 HCAPLUS
(8) Fodor, S; Nature 1993, V364, P555 MEDLINE
(9) Fodor, S; Science 1991, V251, P767 HCAPLUS
(10) Gingeras, T; Genome Res 1998, V8, P435 HCAPLUS
(11) Hacia, J; Nat Genet 1996, V14, P441 HCAPLUS
(12) Hacia, J; Nat Genet 1998, V18, P155 HCAPLUS
(13) Hudson, T; Science 1995, V270, P1945 HCAPLUS
(14) Kozal, M; Nat Med 1996, V2, P753 HCAPLUS
(15) Kruglyak, L; Am J Hum Genet 1996, V58, P1347 HCAPLUS
(16) Kruglyak, L; Nat Genet 1997, V17, P21 HCAPLUS

(17) Kwok, P; Genomics 1996, V31, P123 HCAPLUS
(18) Lander, E; Nat Genet 1995, V11, P241 HCAPLUS
(19) Lander, E; Science 1996, V274, P536 HCAPLUS
(20) Lipshutz, R; Biotechniques 1995, V19, P442 HCAPLUS
(21) Lockhart, D; Nat Biotechnol 1996, V14, P1675 HCAPLUS
(22) Risch, N; Science 1996, V273, P1516 HCAPLUS
(23) Rozen, S; http://www-genome.wi.mit.edu/genome_software/other/primer3.html 1997
(24) Sapolsky, R; Genomics 1996, V33, P445 HCAPLUS
(25) Shoemaker, D; Nat Genet 1996, V14, P450 HCAPLUS
(26) Wang, D; Science 1998, V280, P1077 HCAPLUS
(27) Wodicka, L; Nat Biotechnol 1997, V15, P1359 HCAPLUS

L109 ANSWER 13 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:70377 HCAPLUS
DN 130:120454
TI Method for generating a **high density** linkage disequilibrium-based map of the human **genome**
IN Cohen, Daniel; Blumenfeld, Marta
PA Genset, Fr.
SO Eur. Pat. Appl., 38 pp.
CODEN: EPXXDW
DT Patent
LA English
IC ICM C12Q001-68
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 13
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	EP 892068	A1	19990120	EP 1997-401740	19970718
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	AU 9884569	A1	19990210	AU 1998-84569	19980717
	EP 1002131	A2	20000524	EP 1998-935225	19980717
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI EP 1997-401740 19970718
US 1998-261497 19980421
US 1998-82614 19980421
WO 1998-IB1193 19980717

AB Methods are provided for generating a high d. linkage disequil. map of the human **genome**, markers obtained by the said methods, probes capable of **hybridizing** with the said markers, and primers capable of detecting the said markers, oligonucleotide **arrays** comprising sets of the said probes or primers, diagnostic assay using the said probes and genes identified by the said methods. The method comprises the steps of: (1) ordering a set of 10,000-20,000 cloned **genomic** fragments along the human **genome**, with av. size ranging from 100 kb to 300 kb; (2) generating several bi-allelic markers per fragment; and (3) selecting one to three bi-allelic marker per fragment, with heterozygosity rate >40%. Bi-allelic markers are preferably generated in any region with no evidence of linkage disequil. and in any region with evidence for a pos. assocn. with a genetic trait such as drug response (efficacy, toxicity, and/or tolerance). The high-d. bi-allelic marker map results from the coordinated interaction of 5 fully integrated, industrial scale, methods: oligonucleotide synthesis, high throughput BAC (bacterial artificial chromosome) libraries mapping and subcloning, high throughput **sequencing**, **bioinformatics** anal. and **genomics** anal., including automated microtiter plat microsequencing.

ST linkage disequilibrium **genome** mapping human; biallelic marker **genome** linkage mapping human; BAC biallelic marker **genome** linkage mapping; drug response gene **genome** linkage mapping human
IT Genetic vectors
(BAC (bacterial artificial chromosome); method for generating a high d.

linkage disequil.-based map of the human **genome**)
IT Genetic markers
(bi-allelic; method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Genotyping (method)
(high throughput genotyping of bi-allelic markers by microsequencing; method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Recombination (genetic)
(identification of putative recombination hot spot; method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Diseases (animal)
Drug metabolism
Drug tolerance
Drug toxicity
(identifying genes assocd. with a trait such as disease or drug response; method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Genes (animal)
RL: ANT (Analyte); BOC (Biological occurrence); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence)
(identifying genes assocd. with a trait such as disease or drug response; method for generating a high d. linkage disequil.-based map of the human **genome**)
IT **Genomes**
Genomic library
Linkage (genetic)
(method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Primers (nucleic acid)
Probes (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method for generating a high d. linkage disequil.-based map of the human **genome**)
IT Molecular diagnosis
(oligonucleotide probe or primer for; method for generating a high d. linkage disequil.-based map of the human **genome**)
RE.CNT 11
RE
(1) Chee, M; Science 1996, V274, P610 HCAPLUS
(2) Cox, D; Science 1994, V265, P2031 MEDLINE
(3) Fincham, J; Genetics 1983
(4) Hudson, T; Science 1995, V270, P1945 HCAPLUS
(5) Kim, U; Genomics 1996, V34, P213 HCAPLUS
(6) Kruglyak, L; Nature Genetics 1997, V17(1), P21 HCAPLUS
(7) Lange, K; American Journal of Human Genetics 1991, V49(6), P1320 MEDLINE
(8) Risch, N; Science 1996, V273, P1516 HCAPLUS
(9) Schuler, G; Science 1996, V274, P540 HCAPLUS
(10) Syvanen, A; American Journal of Human Genetics 1993, V52(1), P46 HCAPLUS
(11) Wang, D; American Journal of Human Genetics 1996, V59, PA3

L109 ANSWER 14 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:60020 HCAPLUS
DN 130:232948
TI Strategies for mutational analysis of the large multiexon ATM gene using **high-density** oligonucleotide **arrays**
AU Hacia, Joseph G.; Sun, Bryan; Hunt, Nathaniel; Edgemon, Keith; Mosbrook, Deborah; Robbins, Christiane; Fodor, Stephen P. A.; Tagle, Danilo A.; Collins, Francis S.
CS National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, 20892, USA
SO Genome Res. (1998), 8(12), 1245-1258
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press

DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
AB Mutational anal. of large genes with complex **genomic** structures plays an important role in medical genetics. Tech. limitations assocd. with current mutation screening protocols have placed increased emphasis on the development of new technologies to simplify these procedures. High-d. **arrays** of >90,000-oligonucleotide probes, 25 nucleotides in length, were designed to screen for all possible heterozygous germ-line mutations in the 9.17-kb coding region of the ATM gene. A strategy for rapidly developing multiexon PCR amplification protocols in DNA chip-based **hybridization** anal. was devised and implemented in prepg. target for the 62 ATM coding exons. Improved algorithms for interpreting data from two-color expts., where ref. and test samples are cohybridized to the **arrays**, were developed. In a blinded study, 17 of 18 distinct heterozygous and 8 of 8 distinct homozygous **sequence** variants in the assayed region were detected accurately along with five false-pos. calls while scanning >200 kb in 22 **genomic** DNA samples. Of eight heterozygous **sequence** changes found in more than one sample, six were detected in all cases. Five previously unreported **sequence** changes, not found by other mutational scanning methodologies on these same samples, were detected that led to either amino acid changes or premature truncation of the ATM protein. DNA chip-based assays should play a valuable role in high throughput **sequence** anal. of complex genes.
ST mutation analysis ATM gene oligonucleotide **array**
IT Genes (animal)
RL: ADV (Adverse effect, including toxicity); PRP (Properties); BIOL (Biological study)
(ATM; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT DNA-DNA **hybridization**
(chip-based; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT Proteins (specific proteins and subclasses)
RL: ADV (Adverse effect, including toxicity); ARU (Analytical role, unclassified); ANST (Analytical study); BIOL (Biological study)
(gene ATM; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT PCR (polymerase chain reaction)
(multiplex; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT Mutation
(screening; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT DNA **sequence** analysis
Genetic diagnosis
(strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT Exon (genetic element)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)
IT Ataxia telangiectasia
(strategies for mutational anal. of large multiexon ataxia telangiectasia gene ATM using high-d. oligonucleotide **arrays**)
IT 208880-67-5 208880-69-7 208880-70-0 208881-33-8 221271-96-1
221271-97-2 221271-98-3 221271-99-4 221272-00-0 221272-01-1
221272-02-2 221272-03-3 221272-04-4 221272-05-5 221272-06-6

221272-07-7 221272-08-8 221272-09-9 221272-10-2 221272-12-4
221272-14-6 221272-18-0 221272-20-4 221272-22-6 221272-24-8
221272-25-9 221272-26-0 221272-27-1 221272-28-2 221272-29-3
221272-30-6 221272-31-7 221272-32-8 221272-33-9 221272-35-1
221272-38-4 221272-40-8 221272-41-9 221272-44-2 221272-49-7
221272-51-1 221272-53-3 221272-54-4 221272-55-5 221272-56-6
221272-57-7 221305-21-1 221305-22-2 221305-23-3 221305-24-4
221305-25-5 221305-27-7 221305-29-9 221305-33-5 221305-34-6
221305-35-7 221305-36-8 221305-38-0 221305-39-1 221305-42-6
221305-47-1 221305-50-6 221305-51-7 221305-52-8 221305-53-9
221305-54-0 221305-55-1 221305-56-2 221305-57-3 221305-58-4
221305-61-9 221305-63-1 221305-64-2 221305-65-3 221305-66-4
221305-67-5 221305-68-6 221305-71-1 221305-73-3 221305-74-4
221305-75-5 221305-77-7 221305-81-3 221305-82-4 221305-83-5
221305-84-6 221305-85-7 221305-86-8 221305-87-9 221305-88-0
221305-89-1 221305-90-4 221305-91-5 221305-92-6 221305-93-7
221305-94-8 221305-95-9 221305-96-0 221305-97-1 221305-98-2
221305-99-3 221306-00-9 221306-01-0 221306-02-1 221306-03-2
221306-04-3 221306-05-4 221306-06-5 221306-07-6 221306-08-7
221306-09-8 221306-10-1 221306-11-2 221306-12-3 221306-13-4
221306-14-5 221306-15-6 221306-16-7 221306-17-8 221306-18-9
221306-19-0 221306-21-4 221306-25-8
RL: ARG (Analytical reagent use); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(primer; strategies for mutational anal. of large multiexon ATM gene using high-d. oligonucleotide **arrays**)

RE.CNT 37

RE

(1) Athma, P; Cancer Genet Cytogenet 1996, V92, P130 MEDLINE
(2) Bishop, D; Nature Genet 1997, V16, P226
(3) Branham, R; Scientific data analysis:An introduction to overdetermined systems 1990
(4) Chee, M; Science 1996, V274, P610 HCAPLUS
(5) Cronin, M; Hum Mut 1996, V7, P244 HCAPLUS
(6) Easton, D; Int J Radiat Biol 1994, V66, P177
(7) Fitzgerald, M; Nature Genet 1997, V15, P307 HCAPLUS
(8) Fodor, S; Science 1991, V251, P767 HCAPLUS
(9) Gilad, S; Am J Hum Genet 1998, V62, P551 HCAPLUS
(10) Gilad, S; Hum Mol Genet 1996, V5, P2033 HCAPLUS
(11) Gilad, S; Hum Mol Genet 1996, V5, P433 HCAPLUS
(12) Gilad, S; Hum Mutat 1998, V11, P69 HCAPLUS
(13) Gingeras, T; Genome Res 1998, V8, P435 HCAPLUS
(14) Hacia, J; Breast Disease 1998, V10, P45 HCAPLUS
(15) Hacia, J; Nat Genet 1996, V14, P441 HCAPLUS
(16) Hacia, J; Nat Genet 1998, V18, P155 HCAPLUS
(17) Hacia, J; Nucleic Acids Res 1998, V26, P4975 HCAPLUS
(18) Kozal, M; Nature Med 1996, V2, P753 HCAPLUS
(19) Larson, G; Genet Testing 1998, V1, P165 MEDLINE
(20) Lockhart, D; Nat Biotechnol 1996, V14, P1675 HCAPLUS
(21) McGall, G; J Am Chem Soc 1997, V119, P5081 HCAPLUS
(22) Milner, N; Nat Biotechnol 1997, V15, P537 HCAPLUS
(23) Platzer, M; Genome Res 1997, V7, P592 HCAPLUS
(24) Ramsey, G; Nat Biotechnol 1998, V16, P40
(25) Saenger, W; Principles of nucleic acid structure 1984
(26) Savitsky, K; Nucleic Acids Res 1997, V25, P1678 HCAPLUS
(27) Savitsky, K; Science 1995, V268, P1749 HCAPLUS
(28) Shoemaker, D; Nat Genet 1996, V14, P450 HCAPLUS
(29) Stilgenbauer, S; Nat Med 1997, V3, P1155 HCAPLUS
(30) Swift, M; N Engl J Med 1987, V316, P1289 MEDLINE
(31) Telatar, M; Am J Hum Genet 1996, V59, P40 HCAPLUS
(32) Telatar, M; Am J Hum Genet 1998, V62, P86 HCAPLUS
(33) Vorechovsky, I; Cancer Res 1996, V56, P2276
(34) Wang, D; Science 1998, V280, P1077 HCAPLUS
(35) Wright, J; Am J Hum Genet 1996, V59, P839 HCAPLUS
(36) Yershov, G; Proc Natl Acad Sci 1996, V93, P4913 HCAPLUS
(37) Zuker, M; Methods Mol Biol 1994, V25, P267 HCAPLUS

L109 ANSWER 15 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:53122 HCAPLUS
DN 130:247490
TI **High density** synthetic oligonucleotide **arrays**
AU Lipshutz, Robert J.; Fodor, Stephen P. A.; Gingeras, Thomas R.; Lockhart, David J.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Nat. Genet. (1999), 21(1, Suppl.), 20-24
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
AB A review, with 32 refs. Exptl. **genomics** involves taking advantage of **sequence** information to investigate and understand the workings of genes, cells and organisms. We have developed an approach in which **sequence** information is used directly to design high-d., two-dimensional **arrays** of synthetic oligonucleotides. The **GeneChip** probe **arrays** are made using spatially patterned, light-directed combinatorial chem. synthesis, and contain up to hundreds of thousands of different oligonucleotides on a small glass surface. The **arrays** have been designed and used for quant. and highly parallel measurements of gene expression, to discover polymorphic loci and to detect the presence of thousands of alternative alleles. Here, we describe the fabrication of the **arrays**, their design and some specific applications to high-throughput genetic and cellular anal.
ST review oligonucleotide **array** probe **hybridization**
IT Nucleic acid **hybridization**
(high d. synthetic oligonucleotide **arrays**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(high d. synthetic oligonucleotide **arrays**)
RE.CNT 32
RE
(1) Beecher, J; Polymeric Materials Science & Engineering 1997, V76, P597 HCAPLUS
(2) Bowtell, D; Nature Genet 1999, V21, P25 HCAPLUS
(3) Chakravarti, A; Nature Genet 1999, V21, P56 HCAPLUS
(4) Chee, M; Science 1996, V274, P610 HCAPLUS
(5) Cheung, V; Nature Genet 1999, V21, P15 HCAPLUS
(6) Cho, R; Mol Cell 1998, V2, P65 HCAPLUS
(7) Cho, R; Proc Natl Acad Sci USA 1998, V95, P3752 HCAPLUS
(8) de Saizleu, A; Nature Biotechnol 1998, V16, P45
(9) Duggan, D; Nature Genet 1999, V21, P10 HCAPLUS
(10) Fodor, S; Nature 1993, V364, P555 MEDLINE
(11) Fodor, S; Science 1991, V251, P767 HCAPLUS
(12) Fodor, S; Science 1997, V277, P393 HCAPLUS
(13) Gingeras, T; Genome Res 1998, V8, P435 HCAPLUS
(14) Gray, N; Science 1998, V281, P533 HCAPLUS
(15) Gunderson, K; Genome Res (in press)
(16) Gunthard, H; AIDS Res Hum Retroviruses 1998, V14, P869 HCAPLUS
(17) Hacia, J; Nature Genet 1999, V21, P42 HCAPLUS
(18) Kozal, M; Nature Med 1996, V7, P753
(19) Lockhart, D; Nature Biotechnol 1996, V14, P1675 HCAPLUS
(20) Mack, D; Biology of Tumors 1998, P85 HCAPLUS
(21) McGall, G; J Am Chem Soc 1997, V119, P5081 HCAPLUS
(22) McGall, G; Proc Natl Acad Sci USA 1996, V93, P13555 HCAPLUS
(23) Pease, A; Proc Natl Acad Sci USA 1994, V91, P5022 HCAPLUS
(24) Pirrung, M; J Organic Chem 1998, V63, P241 HCAPLUS
(25) Sapolsky, R; Genomics 1996, V33, P445 HCAPLUS
(26) Shoemaker, D; Nature Genet 1996, V14, P450 HCAPLUS
(27) Southern, E; Genomics 1992, V13, P1008 HCAPLUS
(28) Troesch, A; J Clin Microbiol (in press)
(29) Wang, D; Science 1998, V280, P1077 HCAPLUS

(30) Winzeler, E; Science 1998, V281, P1194 HCAPLUS
(31) Wodicka, L; Nature Biotechnol 1997, V15, P1359 HCAPLUS
(32) Zhu, H; Proc Natl Acad Sci USA (in press)

L109 ANSWER 16 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:46849 HCAPLUS
DN 130:262729
TI Mycobacterium species identification and rifampin resistance testing with **high-density** DNA probe **arrays**
AU Troesch, A.; Nguyen, H.; Miyada, C. G.; Desvarenne, S.; Gingeras, T. R.; Kaplan, P. M.; Cros, P.; Mabilat, C.
CS bioMerieux, Marcy-L'Etoile, 69280, Fr.
SO J. Clin. Microbiol. (1999), 37(1), 49-55
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 10, 14
AB Species identification within the genus Mycobacterium and subsequent antibiotic susceptibility testing still rely on time-consuming, culture-based methods. Despite the recent development of DNA probes, which greatly reduce assay time, there is a need for a single platform assay capable of answering the multitude of diagnostic questions assocd. with this genus. We describe the use of a DNA probe **array** based on two **sequence** databases: one for the species identification of mycobacteria (82 unique 16S rRNA **sequences** corresponding to 54 phenotypical species) and the other for detecting Mycobacterium tuberculosis rifampin resistance (rpoB alleles). Species identification or rifampin resistance was detd. by **hybridizing** fluorescently labeled, amplified genetic material generated from bacterial colonies to the **array**. Seventy mycobacterial isolates from 27 different species and 15 rifampin-resistant M. tuberculosis strains were tested. A total of 26 of 27 species were correctly identified as well as all of the rpoB mutants. This parallel testing format opens new perspectives in terms of patient management for bacterial diseases by allowing a no. of genetic tests to be simultaneously run.
ST PCR detection Mycobacterium tuberculosis rifampin resistance
IT Antibiotic resistance
Mycobacterium
Mycobacterium tuberculosis
Tuberculosis
(Mycobacterium species identification and rifampin resistance testing with high-d. DNA probe **arrays**)
IT 16S rRNA
RL: ANT (Analyte); ANST (Analytical study)
(Mycobacterium species identification and rifampin resistance testing with high-d. DNA probe **arrays**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(Mycobacterium species identification and rifampin resistance testing with high-d. DNA probe **arrays**)
IT Genes (microbial)
RL: ANT (Analyte); ANST (Analytical study)
(rpoB; Mycobacterium species identification and rifampin resistance testing with high-d. DNA probe **arrays**)
IT 13292-46-1, Rifampin
RL: BAC (Biological activity or effector, except adverse); BIOL (Biological study)
(resistance to; Mycobacterium species identification and rifampin resistance testing with high-d. DNA probe **arrays**)
RE.CNT 31
RE
(1) Banerjee, A; Science 1994, V263, P227 HCAPLUS

(2) Boddinghaus, B; J Clin Microbiol 1990, V28, P1751 MEDLINE
(3) Chee, M; Science 1996, V274, P610 HCAPLUS
(4) Cole, S; Trends Microbiol 1994, V2, P411 MEDLINE
(5) Cooksey, R; J Clin Microbiol 1997, V35, P1281 HCAPLUS
(6) Cronin, M; Hum Mutat 1996, V7, P244 HCAPLUS
(7) Fodor, S; Nature 1993, V364, P555 MEDLINE
(8) Gingeras, T; Genome Res 1998, V8, P435 HCAPLUS
(9) Heym, B; Mol Microbiol 1995, V15, P235 HCAPLUS
(10) Horsburgh, C; N Engl J Med 1991, V324, P1332
(11) Jenkins, P; J Appl Bacteriol Symp 1991, V70(Suppl), P137S
(12) Kapur, V; J Clin Microbiol 1994, V32, P1095 HCAPLUS
(13) Kent, P; Public health mycobacteriology:a guide for the level III laboratory 1985
(14) Kirschner, P; J Clin Microbiol 1993, V31, P2882 HCAPLUS
(15) Kirschner, P; J Clin Microbiol 1996, V34, P304 HCAPLUS
(16) Koukila-Kahkola, P; Int J Syst Bacteriol 1995, V45, P549 MEDLINE
(17) Kozal, M; Nat Med 1996, V2, P753 HCAPLUS
(18) Lockhart, D; Nat Biotechnol 1996, V14, P1675 HCAPLUS
(19) Mdluli, K; Science 1998, V280, P1607 HCAPLUS
(20) Raviglione, M; JAMA 1995, V273, P220 MEDLINE
(21) Roberts, G; Manual of clinical microbiology 1991, V5th ed, P304
(22) Scorpio, A; Nat Med 1996, V2, P662 HCAPLUS
(23) Springer, B; J Clin Microbiol 1996, V34, P296 HCAPLUS
(24) Sreevatsan, S; Antimicrob Agents Chemother 1997, V41, P1677 HCAPLUS
(25) Sreevatsan, S; Antimicrob Agents Chemother 1997, V41, P636 HCAPLUS
(26) Telenti, A; Lancet 1993, V341, P647 HCAPLUS
(27) Tortoli, E; J Clin Microbiol 1997, V35, P697 HCAPLUS
(28) Whelen, A; J Clin Microbiol 1995, V33, P556 HCAPLUS
(29) Wilson, T; Mol Microbiol 1996, V19, P1025 HCAPLUS
(30) Yates, M; Int J Tuberc Lung Dis 1997, V1, P75 MEDLINE
(31) Zhang, Y; Nature 1992, V358, P501

L109 ANSWER 17 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:798284 HCAPLUS
DN 130:192430
TI Deciphering molecular circuitry using **high-density** DNA **arrays**
AU Mack, David H.; Tom, Edward Y.; Mahadev, Mamatha; Dong, Helin; Mittmann, Michael; Dee, Suzanne; Levine, Arnold J.; Gingeras, Thomas R.; Lockhart, David J.
CS Program in Cancer Biology, Santa Clara, CA, 95051, USA
SO Pezcoller Found. Symp. (1998), 9(Biology of Tumors), 85-108
CODEN: PFSYES; ISSN: 0961-785X
PB Plenum Publishing Corp.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 14
AB DNA **arrays** contg. oligonucleotides complementary to > 6,500 human EST's were used to generate normal and breast cancer specific gene expression profiles. More than 1,500 expressed genes were detected in both cell types. Over 300 genes demonstrated significantly different levels of expression between normal and transformed cells. Increased mRNA levels were obsd. for the Her2/neu oncogene and genes involved in tis signal transduction, including Grb-7, Ras, Raf, Mek, and ERK. In addn., a simple categorization of the expression changes revealed patterns characteristic of loss of wild-type p53 function. Genotyping of the p53 locus using a DNA resequencing **array** reveled inactivating mutation in the p53 DNA-binding domain and loss of heterogeneity. These data demonstrate a general **array-hybridization** approach to deciphering biochem. pathways and generating testable hypotheses concerning the mechanisms of cell growth and differentiation.
ST DNA **array hybridization** human EST; breast cancer gene expression DNA **array**
IT Genes (animal)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST

(Analytical study); BIOL (Biological study)
(ERK; deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT Genes (animal)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(GRB-7; deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT Genes (animal)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(MEK1; deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT Breast tumors
DNA-DNA **hybridization**
Gene expression
Genotyping (method)
Transformation (neoplastic)
(deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT EST (expressed **sequence** tag)
Oncogenes (animal)
c-Ki-ras gene (animal)
c-erbB2 gene (animal)
neu (receptor)
p21c-Ki-ras protein
p53 (protein)
p53 gene (animal)
raf-1 (protein)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT Proteins (specific proteins and subclasses)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(gene GRB-7; deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT Genes (animal)
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(raf; deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
IT 139691-76-2, GENE RAF-1 PROTEIN KINASE 140034-75-9, GenBank X03484
140743-97-1, GenBank M11730 140796-78-7, GenBank M54968 142243-02-5
146410-92-6, MEK1 protein kinase 148636-91-3, GenBank L11284
155713-83-0, GenBank D31661 160475-87-6, GenBank D43772
RL: ADV (Adverse effect, including toxicity); ANT (Analyte); ANST (Analytical study); BIOL (Biological study)
(deciphering mol. circuitry using high-d. DNA **arrays** in generation of gene expression profiles for normal and breast cancer cells)
RE.CNT 32
RE
(1) Adams, M; Nature 1995, V377, P3 HCAPLUS
(2) Alblas, J; Journal of Biological Chemistry 1993, V30, P22235
(3) Boguski, M; Nature Genetics 1993, V4, P332 HCAPLUS
(4) Chee, M; Science 1996, V5287, P610
(5) Clark, G; Breast Cancer Research and Treatment 1995, V1, P133

(6) Coussens, L; Science 1985, V4730, P1132
(7) Earp, H; Breast Cancer Research and Treatment 1995, V1, P115
(8) Fodor, S; Science 1991, V251, P767 HCAPLUS
(9) Hackett, A; Journal of the National Cancer Institute 1977, V6, P1795
(10) King, C; Science 1985, V4717, P974
(11) Koleske, A; Proceedings of the National Academy of Sciences of the United States of America 1995, V5, P1381
(12) Kraus, M; Proceedings of the National Academy of Sciences of the United States of America 1989, V23, P9193
(13) Lasfargues, E; Journal of the National Cancer Institute 1978, V4, P967
(14) Lemoine, N; British Journal of Cancer 1992, V6, P1116
(15) Levine, A; Cell 1997, V3, P323
(16) Li, N; Nature 1993, V6424, P85
(17) Li, S; Journal of Biological Chemistry 1995, V26, P15693
(18) Lisanti, M; Molecular Membrane Biology 1995, V1, P121
(19) Lockhart, D; Nature Biotechnology 1996, V13, P1675
(20) Marshall, M; Faseb Journal 1995, V13, P1311
(21) Schena, M; Science 1995, V270, P467 HCAPLUS
(22) Sivaraman, V; J Clin Invest 1997, V99(7), P1478 HCAPLUS
(23) Slamon, D; Science 1987, V4785, P177
(24) Slamon, D; Science 1989, V4905, P707
(25) Stein, D; EMBO J 1994, V13, P1331 HCAPLUS
(26) Styles, J; International Journal of Cancer 1990, V2, P320
(27) Van Biesen, T; Nature 1995, V6543, P781
(28) Velculescu, V; Clinical Chemistry 1996, V6 Pt 1, P858
(29) Velculescu, V; Science 1995, V270, P484 HCAPLUS
(30) Wallasch, C; EMBO J 1995, V14, P4267 HCAPLUS
(31) Winitz, S; Journal of Biological Chemistry 1993, V26, P19196
(32) Zhang, L; Science 1997, V276, P1268 HCAPLUS

L109 ANSWER 18 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:746382 HCAPLUS
DN 130:105812
TI A method for global protein expression and antibody screening on **high-density** filters of an **arrayed** cDNA library
AU Bussow, Konrad; Cahill, Dolores; Nietfeld, Wilfried; Bancroft, David; Scherzinger, Eberhard; Lehrach, Hans; Walter, Gerald
CS Max Planck Institute for Molecular Genetics, Berlin, D-14195, Germany
SO Nucleic Acids Res. (1998), 26(21), 5007-5008
CODEN: NARHAD; ISSN: 0305-1048
PB Oxford University Press
DT Journal
LA English
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 6, 15
AB We have developed a technique to establish catalogues of protein products of **arrayed** cDNA clones identified by DNA **hybridization** or **sequencing**. A human fetal brain cDNA library was directionally cloned in a bacterial vector that allows IPTG-inducible expression of His6-tagged fusion proteins. Using robot technol., the library was **arrayed** in microtiter plates and gridded onto high-d. in situ filters. A monoclonal antibody recognizing the N-terminal RGSH6 **sequence** of expressed proteins (RGS.cntdot.His antibody, Qiagen) detected 20% of the library as putative expression clones. Two example genes, GAPDH and HSP90.alpha., were identified on high-d. filters using DNA probes and antibodies against their proteins.
ST protein expression antibody screening **arrayed** cDNA library
IT Genes (animal)
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified); BIOL (Biological study); PREP (Preparation); USES (Uses)
(GAPDH, identification of cDNA clones for; by method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Genes (animal)
RL: BPN (Biosynthetic preparation); BUU (Biological use, unclassified);

BIOL (Biological study); PREP (Preparation); USES (Uses)
(HSP90.alpha., identification of cDNA clones for; by method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Protein HSP90
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(hsp 90.alpha., identification of cDNA clones expressing; method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Probes (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(in method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Gene expression
Immunoassay
Molecular cloning
cDNA library
(method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Proteins (general), preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT Antibodies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT 219710-86-8
RL: PRP (Properties)
(amino acid **sequence**; by method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT 9001-50-7P, Glyceraldehyde-3-phosphate dehydrogenase
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(identification of cDNA clones expressing; method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT 9073-60-3, Penicillinase
RL: PRP (Properties)
(method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
IT 211159-45-4, GenBank AF074376
RL: BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide **sequence**; ion method for global protein expression and antibody screening on high-d. filters of an **arrayed** cDNA library)
RE.CNT 7
RE
(1) Anon; The QIAexpressionist 3rd Ed 1997, P31
(2) Brinkmann, U; Gene 1989, V85, P109 HCAPLUS
(3) Lehrach, H; Interdisciplinary Science Reviews 1997, V22, P37
(4) Maier, E; Nucleic Acids Res 1994, V22, P3423 HCAPLUS
(5) Meier, E; Nucleic Acids Res 1998, V26, P2216
(6) Sparks, A; Nature Biotechnol 1996, V14, P741 HCAPLUS
(7) Young, R; Proc Natl Acad Sci USA 1983, V80, P1194 HCAPLUS

L109 ANSWER 19 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:630137 HCAPLUS
DN 130:859
TI Large-scale expression measurement by **hybridization** methods:

from **high-density** membranes to "DNA chips"
AU Jordan, Bertrand R.
CS TAGC Group, ICIM, Centre d'Immunologie INSERM/CNRS, Marseille, 13288, Fr.
SO J. Biochem. (Tokyo) (1998), 124(2), 251-258
CODEN: JOBIAO; ISSN: 0021-924X
PB Japanese Biochemical Society
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 9
AB A review with 30 refs. The vast amt. of **sequence** information becoming available on genes from man and from other species calls for corresponding increases in the rate of collection for data of a more functional nature. Expression measurements often constitute a first step in this direction, and can be performed on a reasonably large scale using highly parallel **hybridization** methods. Large sets of targets (clones, inserts, oligonucleotides) are **hybridized** with labeled complex probes prepd. from total cell or organ mRNA; under the proper conditions, signals measure the relative abundance of each **sequence** species, and can be acquired quant. These techniques are presently available in three formats: high-d. membranes to be **hybridized** with radioactive complex probes, **microarrays** of DNA spots (a miniaturized version of the former technique) using fluorescent complex probes, and oligonucleotide chips that, although developed originally for mutation detection, can be adapted to perform expression measurements. The miniaturized formats clearly represent the future, since they allow higher sensitivity, assay of large nos. of entities and hopefully provide the opportunity to use small amts. of starting material.
ST review gene expression measurement **hybridization; high density** membrane **hybridization** review; DNA chip **hybridization** gene expression review; oligonucleotide chip **hybridization** gene expression review
IT Gene expression
Nucleic acid **hybridization**
(gene expression detection by **hybridization** methods using high d. membranes, **microarrays** of DNA spots, and DNA chips)
RE.CNT 30
RE
(1) Anon; http://cmgm.Stanford.EDU/pbrown/
(2) Anon; http://www.ncbi.nlm.nih.gov/dbEST/index.html
(3) Bernard, K; Nucleic Acids Res 1996, V24, P1435 HCAPLUS
(4) Chee, M; Science 1996, V274, P610 HCAPLUS
(5) Chen, J; to be published in Genomics 1998
(6) Clontech; http://www.clontech.com/clontech/Catalog/Hybridization/Atlas.html
(7) DeRisi, J; Nature Genet 1996, V14, P457 HCAPLUS
(8) DeRisi, J; Science 1997, V278, P680 HCAPLUS
(9) Fodor, S; Science 1991, V251, P767 HCAPLUS
(10) Fodor, S; Science 1997, V277, P393 HCAPLUS
(11) Genome Systems; http://www.genome-systems.com/GDA/
(12) Granjeaud, S; Genetic Anal Biomol Eng 1996, V12, P151 HCAPLUS
(13) Gress, T; Mamm Genome 1992, V3, P609 HCAPLUS
(14) IMAGE; http://www-bio.llnl.gov/bbrp/image/image.html
(15) Khrapko, K; DNA Seq 1991, V1, P375 HCAPLUS
(16) Lennon, G; Trends Genet 1991, V7, P314 HCAPLUS
(17) Liang, P; Science 1992, V257, P967 HCAPLUS
(18) Lockhart, D; Nature Biotechnol 1996, V14, P1675 HCAPLUS
(19) Nguyen, C; Genomics 1995, V29, P207 HCAPLUS
(20) Okubo, K; Nature Genet 1992, V2, P173 HCAPLUS
(21) Pietu, G; Genome Res 1996, V6, P492 HCAPLUS
(22) Rocha, D; Immunogenetics 1997, V46, P142 HCAPLUS
(23) Schena, M; Proc Natl Acad Sci USA 1996, V93, P10614 HCAPLUS
(24) Schena, M; Science 1995, V270, P467 HCAPLUS
(25) Shalon, D; Genome Res 1996, V6, P639 HCAPLUS
(26) Southern, E; Genomics 1992, V13, P1008 HCAPLUS
(27) Synteni; http://www.synteni.com/

(28) Velculescu, V; Science 1995, V270, P484 HCAPLUS
(29) Wodicka, L; Nature Biotechnol 1997, V15, P1359 HCAPLUS
(30) Zhao, N; Gene 1995, V156, P207 HCAPLUS

L109 ANSWER 20 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:455089 HCAPLUS
DN 129:171114
TI Adapting the Biomek 2000 Laboratory Automation Workstation for printing DNA **microarrays**
AU Macas, Jiri; Nouzova, Marcela; Galbraith, David W.
CS Univ. Arizona, Tucson, AZ, USA
SO BioTechniques (1998), 25(1), 106, 108-110
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton Publishing Co.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
AB The Biomek 2000 Lab. Automation Workstation is used for liq. handling and other repetitive operations in many labs. Since it has very good spatial positioning capabilities, we have modified this workstation to deliver samples at **high densities** onto microscope slides to produce DNA **microarrays**. The workstation tool, originally designed for bacterial colony replication, was adapted to carry special printing pins and was further modified to improve its positional accuracy. Software written in the Tool Command Language was concurrently developed to control the movements of the workstation arm during the process of printing. With these modifications, the workstation can reliably deliver individual samples at a spacing of 0.5 mm, corresponding to a total of more than 3000 samples on a single slide. **Arrays** prepd. in this way were successfully tested in **hybridization** expts.
ST printing DNA **microarray** automation app
IT **Computer program**
Printing (nonimpact)
Process automation
(adapting Biomek 2000 Lab. Automation Workstation for printing DNA **microarrays**)
IT Apparatus
(automated; adapting Biomek 2000 Lab. Automation Workstation for printing DNA **microarrays**)
IT DNA
RL: ARG (Analytical reagent use); PNU (Preparation, unclassified); ANST (Analytical study); PREP (Preparation); USES (Uses)
(immobilized; adapting Biomek 2000 Lab. Automation Workstation for printing DNA **microarrays**)

L109 ANSWER 21 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:323255 HCAPLUS
DN 129:1411
TI **High density** immobilization of nucleic acids and apparatus for dispensing nanovolumes of liquids and formation of multielement **arrays**
IN O'Donnell, Maryanne J.; Cantor, Charles R.; Little, Daniel P.; Koster, Hubert
PA Sequenom, Inc., USA; O'Donnell, Maryanne J.; Cantor, Charles R.; Little, Daniel P.; Koster, Hubert
SO PCT Int. Appl., 157 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C07H021-00
ICS C12Q001-68; B01J019-00
CC 3-1 (Biochemical Genetics)
FAN.CNT 6

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9820020	A2	19980514	WO 1997-US20195	19971106

WO 9820020 A3 19981022
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG
US 6024925 A 20000215 US 1997-787639 19970123
AU 9851980 A1 19980529 AU 1998-51980 19971106
EP 937096 A2 19990825 EP 1997-946893 19971106
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO
DE 19782096 T 20000323 DE 1997-19782096 19971106
DE 29724251 U1 20000921 DE 1997-29724251 19971106
DE 29724252 U1 20000921 DE 1997-29724252 19971106
DE 29724250 U1 20001123 DE 1997-29724250 19971106
DE 29724341 U1 20001221 DE 1997-29724341 19971106
NO 9902169 A 19990706 NO 1999-2169 19990504
PRAI US 1996-746055 19961106
US 1997-786988 19970123
US 1997-787639 19970123
US 1997-947801 19971008
DE 1997-78763 19970123
DE 1997-19782096 19971106
WO 1997-US20195 19971106

AB Processes and kits for immobilizing a high d. of nucleic acids on an insol. surface, which are particularly useful for mass spectrometric detection of nucleic acids, are disclosed. **Arrays** contg. the immobilized nucleic acids and use of the immobilized nucleic acids in a variety of solid phase nucleic acid chem. applications, including nucleic acid synthesis (chem. and enzymic), **hybridization** and/or extension, and **sequencing**, are provided. Serial and parallel dispensing tools that can deliver defined vols. of fluid to generate multi-element **arrays** of sample material on a substrate surface are further provided. Tools provided herein can include an assembly of vesicle elements, or pins, wherein each of the pins can include a narrow interior chamber suitable for holding nanoliter vols. of fluid. Methods for dispensing tools that can be employed to generate multi-element **arrays** of sample material on a substrate surface are also provided. The tool can dispense a spot of fluid to a substrate surface by spraying the fluid from the pin, contacting the substrate surface or forming a drop that touches against the substrate surface. The tool can form an **array** of sample material by dispensing sample material in a series of steps, while moving the pin to different locations above the substrate surface to form the sample **array**. The prepd. sample **arrays** may be passed to a plate assembly that disposes the sample **arrays** for anal. by mass spectrometry. Thiol group-contg. DNA was attached to silicon wafers derivatized first by reaction with 3-aminopropyltriethoxysilane, then with N-succinimidyl(4-iodoacetyl)aminobenzoate. DNA immobilized in this way was used as a template for primer extension in order to detect a mutation in the apoE gene using MALDI-TOF spectroscopy. Using the described chem., DNA **arrays** were also created using serial and parallel dispensing tools. MALDI-TOF spectroscopy could be used to detect **hybridization** to specific DNA mols. and to detect primer extension at specific sites. The synthesis of two photocleavable linkers which can be incorporated into oligonucleotides/nucleic acids is given.

ST nucleic acid **high density** immobilization; app nanovol liq dispensing

IT Mutation
(detection of; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT DNA **sequence** analysis

Electrospray ionization mass spectrometry
Fourier transform mass spectrometry
Immobilization (molecular)
Ion cyclotron resonance mass spectrometry
Mass spectrometry
Matrix-assisted laser desorption ionization mass spectrometry
Nucleic acid **hybridization**
Time-of-flight mass spectrometry
(high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT Apparatus
(liq. dispenser; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT Nucleic acids
RL: BPN (Biosynthetic preparation); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation)
(synthesis and **sequencing** of; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT Nucleic acids
RL: RCT (Reactant)
(thiol-contg., immobilization of; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 7440-21-3, Silicon, uses
RL: DEV (Device component use); USES (Uses)
(**arrays** on; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 72252-96-1
RL: RCT (Reactant)
(crosslinker; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 919-30-2, 3-Aminopropyltriethoxysilane
RL: RCT (Reactant)
(for derivatization of substrate; high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 207398-06-9P
RL: BYP (Byproduct); SPN (Synthetic preparation); PREP (Preparation)
(high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 108-24-7, Acetic anhydride 498-02-2 627-18-9, 3-Bromo-1-propanol 18162-48-6, tert-Butyldimethylsilyl chloride 40615-36-9 42454-06-8, 5-Hydroxy-2-nitrobenzaldehyde 89992-70-1, 2-Cyanoethyl-N,N-diisopropylchlorophosphoramidite
RL: RCT (Reactant)
(high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

IT 187794-03-2P 207298-33-7P 207298-34-8P 207298-35-9P 207298-36-0P 207298-37-1P 207298-38-2P 207298-39-3P 207298-40-6P 207298-41-7P 207298-42-8P 207298-43-9P
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation)
(high d. immobilization of nucleic acids and app. for dispensing nanovolumes of liqs. and formation of multielement **arrays**)

L109 ANSWER 22 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:86089 HCAPLUS
DN 128:163326
TI Evolutionary **sequence** comparisons using **high-density** oligonucleotide **arrays**
AU Hacia, Joseph G.; Makalowski, Wojciech; Edgemon, Keith; Erdos, Michael R.; robbins, Christiane M.; Fodor, Stephen P. A.; Brody, Lawrence C.; collins, Francis S.

CS National Human enome Res. Inst., National Inst. Health, Bethesda, MD, 20892, USA
SO Nat. Genet. (1998), 18(2), 155-158
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 6, 13
AB We explored the utility of high-d. oligonucleotide **arrays** (DNA chips) for obtaining **sequence** information from homologous genes in closely related species. Orthologs of the human BRCA1 exon 11, all approx. 3.4 kb in length and ranging from 98.2% to 83.5% nucleotide identity, were subjected to **hybridization**-based and conventional dideoxysequencing anal. Retrospective guidelines for identifying high-fidelity **hybridization**-based **sequence** calls were formulated based upon dideoxysequencing results. Prospective application of these rules yielded base-calling with .gtoreq.98.8% accuracy over orthologous **sequence** tracts shown to have .apprx.99% identity. For higher primate **sequences** with >97% nucleotide identity, based-calling was made with .gtoreq.99.91% accuracy covering a min. 97% of the **sequence**. Using a second-tier confirmatory **hybridization** chip strategy, shown in several cases to confirm the identity of predicted **sequence** changes, the complete **sequence** of the chimpanzee, gorilla and orangutan orthologs should be deducible solely through **hybridization**-based methodologies. Anal. of less highly conserved orthologues can still identify conserved nucleotide tracts of .gtoreq.15 nucleotides and can provide useful information for designing primers. DNA-chip based assays can be a valuable new technol. for obtaining high-throughput cost-effective **sequence** information from related **genomes**.
ST **high density** oligonucleotide **array** DNA evolution
IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(**array**; evolutionary **sequence** comparisons using high-d. oligonucleotide **arrays**)
IT Chimpanzee
Gorilla
Molecular evolution
Orangutan
(evolutionary **sequence** comparisons using high-d. oligonucleotide **arrays**)
IT BRCA1 gene (animal)
RL: ANT (Analyte); ANST (Analytical study)
(evolutionary **sequence** comparisons using high-d. oligonucleotide **arrays**)

L109 ANSWER 23 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:30840 HCAPLUS
DN 128:136902
TI Polynucleotide **arrays** for genetic **sequence** analysis
AU Anderson, Rolfe C.; McGall, Glenn; Lipshutz, Robert J.
CS Affymetrix Inc, Santa Clara, CA, 95051, USA
SO Top. Curr. Chem. (1998), 194(Microsystem Technology in Chemistry and Life Science), 117-129
CODEN: TPCCAQ; ISSN: 0340-1022
PB Springer-Verlag
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB A new paradigm is described for genetic anal. based upon high d. **arrays** of polynucleotide probes. Methods for light-directed polynucleotide **array** synthesis, as well as **array** packaging, sample prepn., **array hybridization**,

epifluorescence confocal scanning, and data anal. are described. Applications to discovery, genotyping, expression, and resequencing are presented.

ST polynucleotide **array** genetic **sequence** analysis; **high density array** polynucleotide probe method

IT Genetic methods
(high d. **arrays** of polynucleotide probes; polynucleotide **arrays** for genetic **sequence** anal.)

IT Photolithography
(light-directed polynucleotide **array** synthesis; polynucleotide **arrays** for genetic **sequence** anal.)

IT DNA **sequence** analysis
Gene expression
Genotyping (method)
Nucleic acid **hybridization**
(polynucleotide **arrays** for genetic **sequence** anal.)

IT Probes (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(polynucleotide **arrays** for genetic **sequence** anal.)

L109 ANSWER 24 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:757153 HCAPLUS
DN 128:44651
TI **Hybridization** buffers and media improving the signal-to-noise ratio for assays on oligonucleotide **arrays**
IN Cronin, Maureen T.; Miyada, Charles Garrett; Trulson, Mark; Gingeras, Thomas R.; Mcgall, Glenn; Robinson, Claire; Oval, Michelle
PA Affymetrix, Inc., USA; Cronin, Maureen T.; Miyada, Charles Garrett; Trulson, Mark; Gingeras, Thomas R.; Mcgall, Glenn; Robinson, Claire; Oval, Michelle
SO PCT Int. Appl., 25 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-68
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
FAN.CNT 7

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9743450	A1	19971120	WO 1997-US8446	19970516
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6045996	A	20000404	US 1996-648709	19960516
	AU 9730090	A1	19971205	AU 1997-30090	19970516
PRAI	US 1996-648709	19960516			
	US 1993-143312	19931026			
	US 1994-284064	19940802			
	WO 1994-US12305	19941026			
	US 1995-510521	19950802			
	US 1995-544381	19951010			
	WO 1997-US8446	19970516			

AB Methods of improving the signal-to-noise ratio in nucleic acid **hybridization** assays on high-d. (>10,000 oligonucleotides/cm2) substrate-bound oligonucleotide **arrays**, such as the Affymetrix DNA Chip, using **hybridization** media that include an isostabilizing agent, a denaturing agent or a renaturation accelerant are described. Media for use with fluorescein-labeled probes are described.

ST **biochip array hybridization** medium; **hybridization high density** oligonucleotide **array** medium

IT Denaturants
(chaotropic, for nucleic acids, in **hybridization** media; **hybridization** buffers and media improving signal-to-noise ratio for assays on oligonucleotide **arrays**)

IT Denaturants
(for nucleic acids, in **hybridization** media;
hybridization buffers and media improving signal-to-noise ratio
for assays on oligonucleotide **arrays**)
IT Proteins (specific proteins and subclasses)
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(gene 32, as renaturation accelerant in **hybridization** assays;
hybridization buffers and media improving signal-to-noise ratio
for assays on oligonucleotide **arrays**)
IT Proteins (specific proteins and subclasses)
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(heterogeneous nuclear RNA-contg. ribonucleoprotein-assocd., A1, as
renaturation accelerant in **hybridization** assays;
hybridization buffers and media improving signal-to-noise ratio
for assays on oligonucleotide **arrays**)
IT Nucleic acid **hybridization**
(**hybridization** buffers and media improving signal-to-noise
ratio for assays on oligonucleotide **arrays**)
IT Probes (nucleic acid)
RL: ARG (Analytical reagent use); ARU (Analytical role, unclassified);
ANST (Analytical study); USES (Uses)
(immobilized **arrays**; **hybridization** buffers and
media improving signal-to-noise ratio for assays on oligonucleotide
arrays)
IT DNA-binding proteins
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(single-stranded DNA-binding, as renaturation accelerant in
hybridization assays; **hybridization** buffers and media
improving signal-to-noise ratio for assays on oligonucleotide
arrays)
IT 50-00-0, Formaldehyde, analysis 56-81-5, Glycerol, analysis 57-13-6,
Urea, analysis 67-68-5, DMSO, analysis 75-12-7, Formamide, analysis
593-84-0, Guanidine thiocyanate
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(as denaturant in **hybridization** assays; **hybridization**
buffers and media improving signal-to-noise ratio for assays on
oligonucleotide **arrays**)
IT 107-43-7, Betaine
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(as isostabilizing agent; **hybridization** buffers and media
improving signal-to-noise ratio for assays on oligonucleotide
arrays)
IT 57-09-0, CTAB 71-44-3, Spermine 124-20-9, Spermidine 1119-94-4, DTAB
25104-18-1, Polylysine 38000-06-5, Polylysine 199946-22-0
RL: ARU (Analytical role, unclassified); MOA (Modifier or additive use);
ANST (Analytical study); USES (Uses)
(as renaturation accelerant in **hybridization** assays;
hybridization buffers and media improving signal-to-noise ratio
for assays on oligonucleotide **arrays**)
IT 2321-07-5, Fluorescein
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(as reporter group; **hybridization** buffers and media improving
signal-to-noise ratio for assays on oligonucleotide **arrays**)

L109 ANSWER 25 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:582333 HCAPLUS
DN 127:243666
TI The application of photolithographic techniques for the fabrication of
high density oligonucleotide **arrays**
AU Beecher, Jody E.; McGall, Glenn H.; Goldberg, Martin J.
CS Affymetrix, Santa Clara, CA, 95051, USA

SO Polym. Mater. Sci. Eng. (1997), 77, 394-395
CODEN: PMSEDG; ISSN: 0743-0515
PB American Chemical Society
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
Section cross-reference(s): 33, 74
AB A review, with 18 refs. The merging of photolithog. techniques and combinatorial chem. has led to development of oligonucleotide **arrays** for **hybridization**-based **sequence** anal. While fabrication of the **arrays** is efficiently accomplished using a direct photolysis approach, higher contrast methods are needed to achieve smaller feature sizes. To accomplish this, the authors developed a chem. amplified photo process employing a photoacid generator, an enhancer, and an acid labile protecting group. This process can be used to synthesize oligonucleotides in yields approaching those attained with traditional oligonucleotide chem. and with features at least as small as 2 .mu., if not smaller.
ST review photolithog oligonucleotide **array** prepn; **sequence** detn oligonucleotide **array** photolithog review
IT Photolithography
(application of photolithog. techniques for fabrication of high d. oligonucleotide **arrays**)
IT Oligonucleotides
RL: ARG (Analytical reagent use); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation); USES (Uses)
(application of photolithog. techniques for fabrication of high d. oligonucleotide **arrays**)
IT DNA **sequence** analysis
RNA **sequence** analysis
(application of photolithog. techniques for fabrication of high d. oligonucleotide **arrays** for **sequence** detn.)

L109 ANSWER 26 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:517576 HCAPLUS
DN 127:186611
TI Determination of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides
IN Lockhart, David J.; Chee, Mark; Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; Matsuzaki, Hajime; McGall, Glenn H.; Barone, Anthony D.
PA Affymetrix, Inc., USA; Lockhart, David J.; Chee, Mark; Gunderson, Kevin; Lai, Chaoqiang; Wodicka, Lisa; Cronin, Maureen T.; Lee, Danny; Tran, Huu M.; et al.
SO PCT Int. Appl., 214 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q001-00
ICS C12Q001-68; C07H021-00
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9727317	A1	19970731	WO 1997-US1603	19970122
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9722533	A1	19970820	AU 1997-22533	19970122
PRAI	US 1996-10471		19960123		

WO 1997-US1603 19970122
OS MARPAT 127:186611
AB A simplified method for identifying differences in nucleic acid abundances (e.g., expression levels) between two or more samples using an **array** of a large no. (e.g. > 1,000) of arbitrarily selected different oligonucleotide probes where the **sequence** and location of each different probe is known. Nucleic acid samples (e.g. mRNA) are **hybridized** to the probe **arrays** and the pattern of **hybridization** is detd. Differences in the **hybridization** patterns between the samples indicates differences in expression of various genes between those samples. Methods of end-labeling a nucleic acid by ligation of a labeled oligonucleotide to it is also described. These methods can be used to detect **hybridization** by making end-labeling of the immobilized probe dependent upon formation of a **hybrid.** For example, if the nucleic acid is an RNA, a labeled oligoribonucleotide can be ligated using an RNA ligase. End-labeling can also be accomplished by with labeled nucleoside triphosphates, and attaching them to the nucleic acid using a terminal transferase.
ST gene expression **high density** oligonucleotide **array; hybridization high density** oligonucleotide **array;** end labeling **hybridization** oligonucleotide **array**
IT DNA **sequence** analysis
(by nucleic acid **hybridization;** detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Gene expression
Nucleic acid **hybridization**
(detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT mRNA
RL: ANT (Analyte); ANST (Analytical study)
(detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT PCR (polymerase chain reaction)
(end-labeling of products from; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Genetic methods
(end-labeling, in detection of **hybrids;** detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT **Computer program**
(for neural net selection of probes for high d. oligonucleotide **arrays;** detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Neural network simulation (physicochemical)
(for selection of probes for high d. oligonucleotide **arrays;** detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Oligonucleotides
Probes (nucleic acid)
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(immobilized **arrays;** detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Library (nucleic acid)
(of arbitrary oligonucleotides; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT Biotinylation
(of **hybridization** probes; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)
IT 461-89-2DP, as-Triazine-3,5[2H,4H]-dione, analogs 194091-66-2P

194091-67-3P
RL: ARU (Analytical role, unclassified); SPN (Synthetic preparation); ANST (Analytical study); PREP (Preparation)
(as fluoresecent reporter moiety in **hybridization**; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 9075-08-5, Restriction endonuclease
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(cleavage of **hybridization** products with, in detection of **hybrids**; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 9015-85-4, DNA ligase 9027-67-2, Nucleotidyltransferase, terminal deoxyribo- 37353-39-2, RNA ligase
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(end-labeling with; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 9003-98-9, DNAse
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(fragmentation of PCR products with, for **hybridization**; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 58-63-9, Inosine
RL: ARU (Analytical role, unclassified); ANST (Analytical study)
(**hybridization** probes contg.; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 9001-78-9
RL: ARG (Analytical reagent use); CAT (Catalyst use); ANST (Analytical study); USES (Uses)
(in sample processing for end-labeling; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 66-97-7D, Psoralen, derivs.
RL: ARU (Analytical role, unclassified); RCT (Reactant); ANST (Analytical study)
(labeling of nucleic acids with; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

IT 61468-90-4 90053-16-0
RL: RCT (Reactant)
(labeling with fluorescein of; detn. of patterns of gene expression by **hybridization** against dense ordered **arrays** of arbitrary oligonucleotides)

L109 ANSWER 27 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:488878 HCAPLUS
TI The application of photolithographic techniques for the fabrication of **high density** oligonucleotide **arrays**.
AU Beecher, Jody E.; McGall, Glenn H.; Goldberg, Martin J.
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Book of Abstracts, 214th ACS National Meeting, Las Vegas, NV, September 7-11 (1997), PMSE-085 Publisher: American Chemical Society, Washington, D. C.
CODEN: 64RNAO
DT Conference; Meeting Abstract
LA English
AB The merging of photolithog. techniques and combinatorial chem. has led to the development of oligonucleotide **arrays** for **hybridization** based **sequence** anal. While fabrication of the **arrays** is efficiently accomplished using a direct photolysis approach, higher contrast methods are needed to achieve smaller feature

sizes. To accomplish this we have developed a chem. amplified photo process employing a photoacid generator, an enhancer and an acid labile protecting group. The process can be used to synthesize oligonucleotides in yields approaching those attained with traditional oligonucleotide chem. and with features at least as small as 2 .mu., if not smaller.

L109 ANSWER 28 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:448477 HCAPLUS
DN 127:157284
TI Direct **hybridization** of large-insert **genomic** clones on **high-density** gridded cDNA filter **arrays**
AU Kern, Suzanne; Hampton, Garret M.
CS Ludwig Institute Cancer Research, La Jolla, CA, USA
SO BioTechniques (1997), 23(1), 120-124
CODEN: BTNQDO; ISSN: 0736-6205
PB Eaton
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB A major challenge to positional cloning approaches is the identification of coding **sequences** within a region of interest. **Hybridization** of **genomic** fragments that represent a cloned contig of a defined **genomic** region on appropriate cDNA libraries theor. represents a direct soln. to this problem. However, this is tech. difficult and in general, success with this approach has been limited to the use of small fragments, such as those cloned in cosmids and phages. Since most phys. maps are composed of **genomic** DNA cloned in vectors with significantly greater insert size capacity, there is a need to develop efficient methods to use these clones directly as **hybridization** probes. Here we describe a highly sensitive protocol for **hybridization** of P1-derived artificial chromosomes (PACs; av. insert size, 120 kb) on a composite, normalized cDNA library comprised of 200,000 clones spotted at high d. on nylon filters. Because limited **sequence** information on >150 000 of these clones is now available in the public domain, pos. **hybridization** results can be rapidly converted to cDNA **sequence** information without recourse to any clone manipulation in the initial phases of a project. Using these protocols, we have been able to reproducibly detect coding exons that constitute as little as 0.2% of the total pAC insert.
ST direct **hybridization** cDNA filter **array**
IT **Genomes**
Nucleic acid **hybridization**
cDNA library
(direct **hybridization** of large-insert **genomic** clones on high-d. gridded cDNA filter **arrays**)
IT cDNA
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(filter **array**; direct **hybridization** of large-insert **genomic** clones on high-d. gridded cDNA filter **arrays**)

L109 ANSWER 29 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:162629 HCAPLUS
TI Synthesis of **high-density** oligonucleotide **arrays** for **hybridization**-based **sequence** analysis.
AU McGall, Glenn H.; Barone, A. Dale; Fidanza, Jacqueline A.; Beecher, Jody E.; Goldberg, Martin J.; Ngo, Nam; Block, Thadeus S.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Book of Abstracts, 213th ACS National Meeting, San Francisco, April 13-17 (1997), ORGN-367 Publisher: American Chemical Society, Washington, D. C.
CODEN: 64AOAA
DT Conference; Meeting Abstract
LA English
AB **Hybridization** to large **arrays** of DNA probes is proving to be a powerful technique for largescale DNA and RNA **sequence**

anal. As the application of this technol. grows, one of the primary challenges will be to increase the d. of **sequence** information encoded in these **arrays**. This presentation will discuss recent advances in the chem. and methods used for high-d. (>106 **sequences** /cm2) **array** fabrication which integrate solid-phase oligonucleotide synthesis with photolithog. techniques adapted from the microelectronics industry.

L109 ANSWER 30 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:749764 HCAPLUS
DN 126:43230
TI Expression monitoring by **hybridization** to **high-density** oligonucleotide **arrays**
AU Lockhart, David J.; Dong, Helin; Byrne, Michael C.; Follettie, Maximillian T.; Gallo, Michael V.; Chee, Mark S.; Mittmann, Michael; Wang, Chunwei; Kobayashi, Michiko; Horton, Heidi; Brown, Eugene L.
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Nat. Biotechnol. (1996), 14(13), 1675-1680
CODEN: NABIF9; ISSN: 1087-0156
PB Nature Publishing Co.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 9
AB The human **genome** encodes approx. 100,000 different genes, and at least partial **sequence** information for nearly all will be available soon. **Sequence** information alone, however, is insufficient for a full understanding of gene function, expression, regulation, and splice-site variation. Because cellular processes are governed by the repertoire of expressed genes, and the levels and timing of expression, it is important to have exptl. tools for the direct monitoring of large nos. of mRNAs in parallel. We have developed an approach that is based on **hybridization** to small, high-d. **arrays** contg. tens of thousands of synthetic oligonucleotides. The **arrays** are designed based on **sequence** information alone and are synthesized in situ using a combination of photolithog. and oligonucleotide chem. RNAs present at a frequency of 1:300,000 are unambiguously detected, and detection is quant. over more than three orders of magnitude. This approach provides a way to use directly the growing body of **sequence** information for highly parallel exptl. investigations. Because of the combinatorial nature of the chem. and the ability to synthesize small **arrays** contg. hundreds of thousands of specifically chosen oligonucleotides, the method is readily scalable to the simultaneous monitoring of tens of thousands of genes.
ST gene expression monitoring density oligonucleotide **array**
IT **Genomes**
(expression monitoring by **hybridization** to high-d. oligonucleotide **arrays**)
IT mRNA
RL: BPR (Biological process); BIOL (Biological study); PROC (Process)
(expression monitoring by **hybridization** to high-d. oligonucleotide **arrays**)
IT Genes (animal)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(expression monitoring by **hybridization** to high-d. oligonucleotide **arrays**)
IT Oligonucleotides
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(expression monitoring by **hybridization** to high-d. oligonucleotide **arrays**)
IT Genetic methods
(high-d. oligonucleotide **array hybridization**; expression monitoring by **hybridization** to high-d. oligonucleotide **arrays**)

L109 ANSWER 31 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:735357 HCAPLUS
DN 126:27376
TI Quantitative phenotypic analysis of yeast deletion mutants using a highly parallel molecular bar-coding strategy
AU Shoemaker, Daniel D.; Lashkari, Deval A.; Morris, Don; Mittmann, Mike; Davis, Ronald W.
CS Beckman Center, Stanford Univ., Stanford, CA, 94305, USA
SO Nat. Genet. (1996), 14(4), 450-456
CODEN: NGENEC; ISSN: 1061-4036
PB Nature Publishing Co.
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 10
AB A quant. and highly parallel method for analyzing deletion mutants has been developed to aid in detg. the biol. function of thousands of newly identified open reading frames (ORFs) in Saccharomyces cerevisiae. This approach uses a PCR targeting strategy to generate large nos. of deletion strains. Each deletion strain is labeled with a unique 20-base tag **sequence** that can be detected by **hybridization** to a high-d. oligonucleotide **array**. The tags serve as unique identifiers (mol. bar codes) that allow anal. of large nos. of deletion strains simultaneously through selective growth conditions. **Hybridization** expts. show that the **arrays** are specific, sensitive and quant. A pilot study with 11 known yeast genes suggests that the method can be extended to include all of the ORFs in the yeast **genome**, allowing whole **genome** anal. with a single selection growth condition and a single **hybridization**.
ST Saccharomyces deletion strain **biochip** bar code; **high density** microchip **array hybridization** barcode; parallel deletion strain generation bar code
IT Genetic markers
(20-base linker tag **sequence** "bar-code"; highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT Nucleic acid bases
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(20-base linker tag **sequence** "bar-code"; highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT Deletion (mutation)
(deletion strain generation; highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT Biotechnology
(high-d. oligonucleotide **array**; highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT DNA-DNA **hybridization**
PCR (polymerase chain reaction)
Saccharomyces cerevisiae
(highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT Oligonucleotides
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(immobilized, high-d. **array**; highly parallel mol. bar-coding strategy for yeast deletion strain generation)
IT Genes (microbial)
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(replacement of; highly parallel mol. bar-coding strategy for yeast deletion strain generation)

L109 ANSWER 32 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:641840 HCAPLUS
DN 125:294156
TI Accessing genetic information with **high-density** DNA **arrays**
AU Chee, Mark; Yang, Robert; Hubbell, Earl; Berno, Anthony; Huang, Xiaohua C.; Stern, David; Winkler, Jim; Lockhart, David J.; Morris, Macdonald S.;

Fodor, Stephen P. A.
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Science (Washington, D. C.) (1996), 274(5287), 610-614
CODEN: SCIEAS; ISSN: 0036-8075
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
AB Rapid access to genetic information is central to the revolution taking place in mol. genetics. The simultaneous anal. of the entire human mitochondrial **genome** is described here. DNA **arrays** contg. up to 135,000 probes complementary to the 16.6-kilobase human mitochondrial **genome** were generated by light-directed chem. synthesis. A two-color labeling scheme was developed that allows simultaneous comparison of a polymorphic target to a ref. DNA or RNA. Complete **hybridization** patterns were revealed in a matter of minutes. **Sequence** polymorphisms were detected with single-base resoln. and unprecedented efficiency. The methods described are generic and can be used to address a variety of questions in mol. genetics including gene expression, genetic linkage, and genetic variability.
ST genetic information **high density** DNA **array**; tiled **array** genetic polymorphism **genome** analysis
IT Genetic polymorphism
Genetics
(accessing genetic information with high-d. DNA **arrays**)
IT Deoxyribonucleic acids
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(accessing genetic information with high-d. DNA **arrays**)
IT **Genome**
(human mitochondrial; accessing genetic information with high-d. DNA **arrays**)
IT Genetic methods
(tiled **array**; accessing genetic information with high-d. DNA **arrays**)
IT Nucleotides, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(oligo-, deoxyribo-, probes, accessing genetic information with high-d. DNA **arrays**)

L109 ANSWER 33 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:147106 HCAPLUS
DN 124:222050
TI From **hybridization** image to numerical values: a practical, high throughput quantification system for **high density** filter **hybridizations**
AU Granjeaud, Samuel; Nguyen, Catherine; Rocha, Dominique; Luton, Robert; Jordan, Bertrand R.
CS Centre d'Immunologie, CNRS, Marseille, 13288, Fr.
SO Genet. Anal.: Biomol. Eng. (1996), 12(3,4), 151-62
CODEN: GEANF4
DT Journal
LA English
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 9
AB **Hybridization** to sets of bacterial colonies or PCR products **arrayed** on high d. filters is used in a no. of exptl. schemes. In many cases it is desirable to collect quant. information ('**hybridization** signatures') rather than indications on 'pos.' and 'neg.' colonies. We present a practical system, based on an imaging plate analyzer and a customized version of com. software, that makes such quantification feasible, and define its performance in terms of reproducibility and linearity. The system is far superior to methods based on autoradiog. and should be useful in many projects that involve the increasingly popular high d. filter format.
ST filter **hybridization** image quantification PCR; software image analysis nucleotide **hybridization** clone

IT Filters and Filtering materials
(high d.; high-throughput quantification system for high-d. filter **hybridizations**)
IT Algorithm
Computer program
Imaging
Molecular cloning
Polymerase chain reaction
(high-throughput quantification system for high-d. filter **hybridizations**)
IT Ribonucleic acids, messenger
RL: ARG (Analytical reagent use); ANST (Analytical study); USES (Uses)
(high-throughput quantification system for high-d. filter **hybridizations**)
IT Nucleic acid **hybridization**
(DNA-RNA, high-throughput quantification system for high-d. filter **hybridizations**)
IT Deoxyribonucleic acids
RL: ANT (Analyte); ANST (Analytical study)
(complementary, high-throughput quantification system for high-d. filter **hybridizations**)

L109 ANSWER 34 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1996:132245 HCAPLUS
DN 124:254790
TI **High-density** gridding: techniques and applications
AU Southern, Edwin M.
CS Dep. Biochem., Univ. Oxford, Oxford, OX1 3QU, UK
SO Curr. Opin. Biotechnol. (1996), 7(1), 85-8
CODEN: CUOBE3; ISSN: 0958-1669
DT Journal; General Review
LA English
CC 9-0 (Biochemical Methods)
AB A review with 21 refs. Much progress has been made in the development of techniques for constructing dense grids either of ligands, such as peptides and oligonucleotides, or of cloned nucleic acids. Such **arrays** are finding practical applications in the anal. of **sequence** variation and gene expression. Methods for carrying out large nos. of analyses in parallel will be essential for the genetic program that is developing from large-scale **sequencing** projects.
ST review **high density** gridding oligonucleotide **hybridization**
IT Nucleic acid **hybridization**
(high-d. gridding)
IT Nucleotides, biological studies
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(oligo-, high-d. gridding)

L109 ANSWER 35 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1994:673167 HCAPLUS
DN 121:273167
TI **Hybridization** techniques on gridded **high density** DNA and in situ colony filters based on fluorescence detection
AU Maier, Elmar; Crollius, Hugues Roest; Lehrach, Hans
CS Genome Anal. Lab., Imperial Cancer Res. Fund, London, WC2A 3PX, UK
SO Nucleic Acids Res. (1994), 22(16), 3423-4
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
CC 3-1 (Biochemical Genetics)
AB In the author's **hybridization**-based approach to **genome** anal., high d. **arrayed** DNA and in situ colony filters are being used to analyze large nos. of clones. Thus far, only hazardous and radioactive labeled probes have been used successfully. However, due to

their low detection resoln., densities of up to 3000 clones per 7.3 cm x 11 cm filter proved to be the limit for reliable automated image anal. The authors describe here **hybridization** techniques on gridded high d. DNA and in situ colony filters using biotin and digoxigellin labeled probes and their detection via the enzyme-linked fluorescence of BBTP. Probes of any length ranging from short oligonucleotides used for **sequence** fingerprinting in cDNA anal. to complex PCR products of YAC clones used in long range mapping have been **hybridized** successfully. This fluorescent based **hybridization** and detection technique has the potential to increase several-fold the throughput of **hybridization** fingerprinting in **genome** anal.

ST DNA **hybridization** method fluorescence fingerprinting **genome**

IT Fluorescence
(detection; fluorescent based **hybridization** and detection technique for high level **genome hybridization** fingerprinting)

IT Deoxyribonucleic acids
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(fluorescent based **hybridization** and detection technique for high level **genome hybridization** fingerprinting)

IT Bond
(**hybridized,** fluorescent based **hybridization** and detection technique for high level **genome hybridization** fingerprinting)

L109 ANSWER 36 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1994:46913 HCAPLUS
DN 120:46913
TI The construction of a human **genome** YAC library and **high density** screening by **hybridization** on membranes spotted in **arrays**
AU Chai, Jianhua; Gu, Yanghong
CS Inst. Genet., Fudan Univ., Shanghai, 200433, Peop. Rep. China
SO Yichuan Xuebao (1993), 20(4), 285-9
CODEN: ICHPCG; ISSN: 0379-4172
DT Journal
LA Chinese
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 13
AB A human **genomic** YAC (yeast artificial chromosome) library was constructed from human white blood cells and the cell line GM1414 contg. 4 X chromosome DNA using pYAC4 as the vector. Twenty thousand YAC clones were obtained with insert sizes of 400 - 1000 kb. A set of YACs contg. the entire dystrophin gene DMD were selected.

ST human **genome** cloning YAC; **hybridization** screening human **genome** YAC; dystrophin gene DMD human YAC clone

IT **Genome**
(construction of YAC library contg. human, selection of gene DMD-contg. clones after)

IT Molecular cloning
(of human **genome,** in YAC library, selection of gene DMD-contg. clones after)

IT Gene, animal
RL: BIOL (Biological study)
(DMD, for dystrophin, of human, YAC clones contg.)

IT Genetic vectors
(YAC, cloning of human **genome** in, selection of gene DMD-contg. clones after)

IT Proteins, specific or class
RL: BIOL (Biological study)
(dystrophins, gene DMD for human, YAC clones contg.)

L109 ANSWER 37 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1992:167187 HCAPLUS

DN 116:167187
TI Automated construction of **high-density** gridded **arrays** of chromosome-specific cosmid libraries
AU Longmire, Jonathan L.; Brown, Nancy C.; Ford, Amanda A.; Naranjo, Cleo M.; Ratliff, Robert L.; Hildebrand, Carl E.; Stallings, Raymond L.; Costa, Anita K.; Avdalovic, Nebojsa; Deaven, Larry L.
CS Genom. Struct. Biol. Group, Los Alamos Natl. Lab., Los Alamos, NM, 87545, USA
SO Lab. Rob. Autom. (1991), 3(4-5), 195-8
CODEN: LRAUEY; ISSN: 0895-7533
DT Journal; General Review
LA English
CC 3-0 (Biochemical Genetics)
AB A review with 7 refs. The Los Alamos National Lab. was selected as one of three sites to beta test a new tool and software package for the Beckman Biomek 1000 designed to construct high-d. gridded **arrays** of cosmid clones. The system is capable of gridding bacterial clones at different densities onto microtiter plate-size agar beds or **hybridization** membranes. **Hybridization** to radiolabeled DNA **sequence** probes produced unambiguous autoradiog. results allowing positional identification of pos. clones on membranes contg. 1536 bacterial colonies. These results demonstrate that it is now feasible to construct high-d. gridded **arrays** of multiple representation chromosome-specific cosmid libraries. Such grids provide a valuable resource for efforts to map human chromosomes as well as a new method for distributing chromosome specific libraries.
ST chromosome cosmid library grid automation review
IT Chromosome
(cosmid libraries specific for, high-d. gridded **arrays** of, automated method for construction of)
IT **Computer program**
(for construction of high-d. gridded **arrays** of cosmid libraries, for specific chromosomes)
IT Nucleic acid **hybridization**
(DNA-DNA, of cosmid libraries of specific chromosomes, automated method for construction of high-d. gridded **arrays** for)
IT Genetic vectors
(cosmid, libraries, of specific chromosomes, construction of high-d. gridded **arrays** of, automated method for)

L109 ANSWER 38 OF 39 HCAPLUS COPYRIGHT 2001 ACS
AN 1991:423587 HCAPLUS
DN 115:23587
TI Construction, **arraying**, and **high-density** screening of large insert libraries of human chromosomes X and 21: their potential use as reference libraries
AU Nizetic, Dean; Zehetner, Gunther; Monaco, Anthony P.; Gellen, Lisa; Young, Bryan D.; Lehrach, Hans
CS Genome Anal. Lab., Imp. Cancer Res. Fund, London, WC2A 3PX, UK
SO Proc. Natl. Acad. Sci. U. S. A. (1991), 88(8), 3233-7
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
CC 3-4 (Biochemical Genetics)
Section cross-reference(s): 13
AB The authors constructed cosmid libraries from flow-sorted human chromosomes X and 21, each of which contains >30 **genome** equiv., and have developed systems allowing permanent storage of primary clones, easy screening of libraries in high-d. filter formats, and the simultaneous generation of fingerprinting and mapping data on the same set of cosmid clones. Clones are picked into microtiter plate wells and stored at -70.degree.. A semiautomatic robot system allows the generation of filter replica contg. up to 10,000 clones per membrane. Sets of membranes contg. 15-20 chromosome equiv. of both chromosomes will be used for the construction of ordered clone libraries by **hybridization** fingerprinting protocols. In addn., multiple sets of two membranes contg.

4 chromosome equiv. of the human X chromosome, and one membrane contg. 3 chromosome equiv. of chromosome 21, have been distributed to other interested labs. as part of a system of ref. libraries. This system allows other groups easy access to the clones and offers an efficient protocol to combine results generated in different labs. using these libraries. The construction of the libraries is described and the use of high-d. screening filters in oligonucleotide probe **hybridizations** and the isolation of cosmids by **hybridization** with probes from the X chromosome is demonstrated.

ST human chromosome X 21 library screening

IT Gene and Genetic element, animal
RL: BIOL (Biological study)
(library of, of human chromosomes X and 21, construction and screening of large insert, human **genome** mapping in relation to)

IT Molecular cloning
(of genes of large inserts of human chromosomes X and 21, construction and screening in relation to)

IT Nucleic acid **hybridization**
(DNA-DNA, of human chromosomes X and 21, ref. library construction and **arraying** and screening in relation to)

IT Plasmid and Episome
(cosmid, library of, of human X and 21 chromosomes, isolation of, construction and screening in relation to)

IT Chromosome
(human 21, gene libraries of, construction and screening of large insert, human **genome** mapping in relation to)

IT Chromosome
(human X, gene libraries of, construction and screening of large insert, human **genome** mapping in relation to)

L109 ANSWER 39 OF 39 HCAPLUS COPYRIGHT 2001 ACS

AN 1982:195370 HCAPLUS

DN 96:195370

TI The covalent structure of apolipoprotein A-I from canine **high density** lipoproteins

AU Chung, Hyangsook; Randolph, Anne; Reardon, Ilene; Heinrikson, Robert L.

CS Dep. Biochem., Univ. Chicago, Chicago, IL, 60637, USA

SO J. Biol. Chem. (1982), 257(6), 2961-7
CODEN: JBCHA3; ISSN: 0021-9258

DT Journal

LA English

CC 6-3 (General Biochemistry)

AB The complete amino acid **sequence** of apolipoprotein A-I (apo-A-I) from canine serum high-d. lipoproteins (HDL) was detd. by automated Edman degrdn. of the intact protein and its proteolytic fragments. Overlapping sets of peptides generated by cleavage at lysyl residues with Myxobacter protease and by tryptic hydrolysis at arginine residues in the citraconylated protein deriv. were analyzed. Canine apo-A-I has 232 residues in its single polypeptide chain, and its covalent structure is highly homologous to 1 of the 2 reported **sequences** for human apo-A-I. As in the human apoprotein, predictive anal. of the canine apo-A-I **sequence** suggests that it comprises a series of amphiphilic .alpha.-helixes punctuated by a periodic **array** of prolyl residues. Canine apo-A-I has all of the structural features of human apo-A-I and is not an A-I:A-II **hybrid** mol.

ST **high density** lipoprotein **sequence**; peptide **sequence** lipoprotein serum dog

IT Dog
(high-d. lipoprotein A-I of serum of, amino acid **sequence** of)

IT Conformation and Conformers
(of high-d. lipoprotein A-I of dog serum)

IT Protein **sequences**
(of high-d. lipoprotein A-I, of dog serum, complete)

IT Lipoproteins
RL: PRP (Properties)
(high-d. apo-, A-I, amino acid **sequence** of, of dog serum)

IT 81726-23-0
RL: PRP (Properties)
(amino acid **sequence** of)

=> d bib abs retable tot

L138 ANSWER 1 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2001:12493 HCAPLUS
TI Human BAP28 gene, cDNA, and protein and markers and methods for diagnosis and treatment of prostate cancer
IN Barry, Caroline; Bougueleret, Lydie; Chumakov, Ilya; Cohen-Akenine, Annick
PA Genset, Fr.
SO PCT Int. Appl., 349 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2001000669	A2	20010104	WO 2000-IB1183	20000623

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-141323 19990625
US 2000-176880 20000118
AB The present invention is directed to BAP28 proteins, BAP28 cDNA sequences encoding BAP28 proteins, to the sequence of the BAP28 gene as well as to regulatory regions located at the 5'- and 3'-ends of the BAP28 coding region. The invention also deals with antibodies directed specifically against such proteins that are useful as diagnostic reagents. The invention further encompasses biallelic markers of the BAP28 gene useful in genetic anal. The invention concerns an assocn. of the BAP28-related biallelic markers with prostate cancer. Therefore, the invention contemplates the diagnostic and treatment methods of prostate cancer. Thus, the BAP28 gene and BAP28 cDNA were cloned and sequenced. The BAP28 gene is found on the antisense strand of the PCTA-1 gene. The BAP28 gene was mapped to human chromosome 1q43. Genetic polymorphisms and their correlation with prostate cancer were detd.

L138 ANSWER 2 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2001:371 HCAPLUS
TI Detection of deleted genomic DNA using a semiautomated computational analysis of **GeneChip** data
AU Salamon, Hugh; Kato-Maeda, Midori; Small, Peter M.; Drenkow, Jorg; **Gingeras, Thomas R.**
CS Division of Infectious Diseases and Geographic Medicine, Dep. of Medicine, Stanford University, Stanford, CA, 94305, USA
SO Genome Res. (2000), 10(12), 2044-2054
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB Genomic diversity within and between populations is caused by single nucleotide mutations, changes in repetitive DNA systems, recombination mechanisms, and insertion and deletion events. The contribution of these sources to diversity, whether purely genetic or of phenotypic consequence, can only be investigated if we have the means to quantitate and characterize diversity in many samples. With the advent of complete

sequence characterization of representative genomes of different species, the possibility of developing protocols to screen for genetic polymorphism across entire genomes is actively being pursued. The large nos. of measurements such approaches yield demand that we pay careful attention to the numerical anal. of data. In this paper we present a novel application of an Affymetrix **GeneChip** to perform genome-wide screens for deletion polymorphism. A **high-d.** oligonucleotide **array** formatted for mRNA expression and targeted at a fully sequenced 4.4-million-base pair Mycobacterium tuberculosis std. strain genome was adapted to compare genomic DNA. Hybridization intensities to 111,000 probe pairs (perfect complement and mismatch complement) were measured for genomic DNA from a clin. strain and from a vaccine organism. Because individual probe-pair hybridization intensities exhibit limited sensitivity/specificity characteristics to detect deletions, data-anal. methodol. to exploit measurements from multiple probes in tandem locations across the genome was developed. The TSTEP (Tandem Set Terminal Extreme Probability) algorithm designed specifically to analyze the tandem hybridization measurements data was applied and shown to discover genomic deletions with high sensitivity. The TSTEP algorithm provides a foundation for similar efforts to characterize deletions in many hybridization measures in similar-sized and larger genomes. Issues relating to the design of genome content screening expts. and the implications of these methods for studying population genomics and the evolution of genomes are discussed.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Behr, M	1999	284	1520	Science	HCAPLUS
Brosch, R	1998	66	2221	Infect Immun	HCAPLUS
Cole, S	1998	393	537	Nature	HCAPLUS
Lipshutz, R	1999	21	20	Nat Genet	HCAPLUS
Mahairas, G	1996	178	1274	J Bacteriol	HCAPLUS
Valway, S	1998	338	633	N Engl J Med	MEDLINE
Winzeler, E	1999	118	S73	Parasitology	HCAPLUS

L138 ANSWER 3 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:881362 HCAPLUS
DN 134:37908
TI Non-cognate hybridization system (NCHS) to probe non-cognate nucleic acid sequences for use in diagnosis
IN Schrenzel, Jacques; Hibbs, Jonathan
PA Switz.
SO PCT Int. Appl., 58 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000075377	A2	20001214	WO 2000-US15893	20000602

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-137327 19990603
AB The present invention comprises a non-cognate hybridization system (NCHS). The NCHS generally includes a hybridization technol. that is simply and economically used to probe for non-cognate nucleic acid sequences, i.e., for nucleic acid strands without known target sequences. NCHS causes nucleic acids, bound to a probe surface, to create a hybridization pattern

that provides information about the presence and/or quantity of the nucleic acid sequences in a sample. The NCHS results normally orient the examiner towards a small no. of specific diagnoses across a wide variety of diagnostic categories (including but not limited to infections, neoplasms and autoimmune diseases). The test will also identify final-common-pathway syndromes such as sepsis, anaphylaxis and tumor necrosis. While the test utilizes genetic information, it does not depend on prior knowledge of the genes involved in a particular disease or syndrome.

L138 ANSWER 4 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:878426 HCAPLUS
TI The transcriptional responses of respiratory epithelial cells to Bordetella pertussis reveal host defensive and pathogen counter-defensive strategies
AU Belcher, Christopher E.; Drenkow, Jorg; Kehoe, Bettina; **Gingeras, Thomas R.**; McNamara, Nancy; Lemjabbar, Hassan; Basbaum, Carol; Relman, David A.
CS Departments of Pediatrics, Stanford University, Stanford, CA, 94305, USA
SO Proc. Natl. Acad. Sci. U. S. A. (2000), 97(25), 13847-13852
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Bordetella pertussis, the causative agent of whooping cough, has many well-studied virulence factors and a characteristic clin. presentation. Despite this information, it is not clear how B. pertussis interaction with host cells leads to disease. In this study, we examd. the interaction of B. pertussis with a human bronchial epithelial cell line (BEAS-2B) and measured host transcriptional profiles by using **high -d.** DNA **microarrays**. The early transcriptional response to this pathogen is dominated by altered expression of cytokines, DNA-binding proteins, and NF.kappa.B-regulated genes. This previously unrecognized response to B. pertussis was modified in similar but nonidentical fashions by the antiinflammatory agents dexamethasone and sodium salicylate. Cytokine protein expression was confirmed, as was neutrophil chemoattraction. We show that B. pertussis induces mucin gene transcription by BEAS-2B cells then counters this defense by using mucin as a binding substrate. A set of genes is described for which the catalytic activity of pertussis toxin is both necessary and sufficient to regulate transcription. Host genomic transcriptional profiling, in combination with functional assays to evaluate subsequent biol. events, provides insight into the complex interaction of host and pathogen.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Aho, S	1997	247	503	Eur J Biochem	HCAPLUS
Anisowicz, A	1991	147	520	J Immunol	HCAPLUS
Boschwitz, J	1997	176	678	J Infect Dis	HCAPLUS
Brockstedt, E	1999	18	225	J Protein Chem	HCAPLUS
Cundell, D	1994	62	639	Infect Immun	HCAPLUS
Detmers, P	1991	147	4211	J Immunol	MEDLINE
Ding, Y	1995	1	279	Oral Dis	MEDLINE
Dohrman, A	1998	1406	251	Biochim Biophys Acta	HCAPLUS
Ebnet, K	1997	158	3285	J Immunol	HCAPLUS
Eckmann, L	2000	275	14084	J Biol Chem	HCAPLUS
Flak, T	2000	68	1235	Infect Immun	HCAPLUS
Gesser, B	1996	59	407	J Leukocyte Biol	HCAPLUS
Grey, S	1999	190	1135	J Exp Med	HCAPLUS
Hammond, M	1995	155	1428	J Immunol	HCAPLUS
Heiss, L	1994	91	267	Proc Natl Acad Sci U	HCAPLUS
Hewlett, E	1985	61	21	Dev Biol Stand	MEDLINE
Ishibashi, Y	1994	180	1225	J Exp Med	HCAPLUS
Ishikawa, H	1987	55	1607	Infect Immun	HCAPLUS
Jinquan, T	1995	155	5359	J Immunol	HCAPLUS

Katada, T	1982	79	3129	Proc Natl Acad Sci U	HCAPLUS
Khelef, N	1995	134	27	FEMS Microbiol Lett	HCAPLUS
Khelef, N	1994	62	2893	Infect Immun	HCAPLUS
Lapin, J	1943			Whooping Cough	
Lechner, J	1985	9	43	J Tissue Culture Met	
Lee, S	1997	185	1275	J Exp Med	HCAPLUS
Matsusaka, T	1993	90	10193	Proc Natl Acad Sci U	HCAPLUS
Pizza, M	1989	246	497	Science	HCAPLUS
Relman, D	1989	86	2637	Proc Natl Acad Sci U	HCAPLUS
Roberts, I	1992	11	982	Pediatr Infect Dis J	MEDLINE
Rollins, B	1991	78	1112	Blood	HCAPLUS
Rosenberger, C	2000	164	5894	J Immunol	HCAPLUS
Saura, M	1998	53	38	Kidney Int	HCAPLUS
Scheinman, R	1995	270	283	Science	HCAPLUS
Spangrude, G	1985	135	4135	J Immunol	HCAPLUS
Tamaoki, J	1997	27	972	Clin Exp Allergy	HCAPLUS
Tokunaga, T	1999	22	745	Biol Pharmacol Bull	HCAPLUS
Uren, A	1996	93	4974	Proc Natl Acad Sci U	HCAPLUS
Vaddi, K	1994	153	4721	J Immunol	HCAPLUS
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS
Wolpe, S	1989	86	612	Proc Natl Acad Sci U	HCAPLUS
Yin, M	1998	396	77	Nature (London)	HCAPLUS
Zhu, H	1998	95	14470	Proc Natl Acad Sci U	HCAPLUS

L138 ANSWER 5 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:850761 HCAPLUS
TI Analysis of drug pharmacology towards predicting drug behavior by expression profiling using **high-density** oligonucleotide **arrays**
AU Hu, Jing-Shan; Durst, Mark; Kerb, Reinhold; Truong, Vivi; Ma, Jing-Tyan; Khurgin, Elina; Balaban, David; **Gingeras, Thomas R.**; Hoffman, Brian B.
CS Affymetrix, Incorporated, Santa Clara, CA, 95051, USA
SO Ann. N. Y. Acad. Sci. (2000), 919(Toxicology for the Next Millennium), 9-15
CODEN: ANYAA9; ISSN: 0077-8923
PB New York Academy of Sciences
DT Journal
LA English
AB An important aspect of the drug development process is prediction of efficacious and toxic side effects. Profiling of mRNA expression is a powerful approach to analyze the mol. phenotype of cells under various conditions, for example, in response to stimulation by compds. We attempt to explore the approach of using expression profiling to identify patterns or fingerprints that are correlated with specific drug properties or behaviors. Identification of such expression patterns may also lead to revelation of the potential action mechanism of drugs and fingerprints indicative of certain drug efficacy or side effects. We describe here a strategy that was used to identify a set of genes whose differential expression pattern correlates with activation mode and target specificity of a specific group of drug compds.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Gabriel, K	1971	58	453	Biometrika	
Johnson, R	1988			Applied Multivariate	
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Wilcox, R	1998	3	2174	Encyclopedia of Bios	
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS

L138 ANSWER 6 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:742291 HCAPLUS
DN 133:318238
TI Method for the analysis of single nucleotide polymorphisms by primer extension techniques in restriction fragments generated using AFLP

IN Kuiper, Marius Tiemen Roelof; Witsenboer, Hanneke
PA Keygene N.V., Neth.
SO PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 2

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000061801	A2	20001019	WO 2000-NL235	20000410

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI EP 1999-201112 19990409
AB A method of detecting single nucleotide polymorphisms (SNP) by primer extension techniques in a mixt. of targeted restriction fragments is described. A mixt. of restriction fragments is hybridized with a probe that is designed to leave an unpaired base at its 3'-end upon hybridization. The hybrids are then incubated with a labeled nucleotide or nucleotide analog in the presence of a polymerase that can fill in the overlap. The incubation products are then analyzed to detect incorporation of the label. The mixt. of restriction fragments used preferably is or has been amplified using AFLP. The method can be adapted to the anal. of SNP in mixts. of fragments using ordered immobilized **arrays** of probes. Use of the method is demonstrated in plant DNA and human DNA such as male-specific Y chromosomal SNP. This particular method for detecting single nucleotide polymorphisms (SNPs) in (const.) AFLP-fragments can be developed into a high throughput DNA marker system for genetic mapping and diagnosis.

L138 ANSWER 7 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:723211 HCAPLUS
DN 133:277154
TI Proportional amplification of nucleic acids by **GeneChip**.RTM. analysis involving a nucleic acid probe **array**
IN Cao, Yanxiang; Mei, Rui; Lockhart, David; Su, Xing
PA Affymetrix, Inc., USA
SO Eur. Pat. Appl., 18 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 1043405	A2	20001011	EP 2000-302761	20000331

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO

JP 2000312585	A2	20001114	JP 2000-104019	20000405

PRAI US 1999-285658 19990405
AB The proportional amplification of nucleic acids can increase the amt. of nucleic acids while preserving the relative abundance of the individual nucleic acid species, or portions thereof, in the original sample. A proportionally amplified nucleic acid prepn. may be analyzed in a gene expression monitoring system, preferably involving a nucleic acid probe **array**.

L138 ANSWER 8 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:688407 HCAPLUS
DN 133:262261
TI Methods for detection of genetic polymorphisms using peptide-labeled

oligonucleotides and antibody **arrays**
IN Treich, Isabelle; Iris, Francois J. M.; Pourny, Jean-louis
PA Valigene Corporation, USA
SO PCT Int. Appl., 62 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000056926	A2	20000928	WO 2000-US6950	20000316

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-272970 19990319
AB The present invention is directed to methods and compns. for use in screening nucleic acid populations for nucleic acid polymorphisms. The methods, referred to generally as ValigeneSM Mutation Screening, Peptide-Linked (VGMS-PL) methods, are specifically designed for high-throughput genotype mapping and gene expression anal. of animal and plant nucleic acids without requiring a PCR amplification step. In particular, the methods of the invention utilize oligonucleotide probes labeled with distinguishable and identifiable peptide tags, that are captured on addressable antibody **arrays**. Mutations can be detected in captured hybrids by screening with reagents such as mismatch-specific nucleases or repair proteins to detect mismatches between a probe derived from a wild-type gene and the target sequence. Hybrids that are cleaved at mismatches can lose an end label and the loss of the label can be detected, e.g. fluorimetrically.

L138 ANSWER 9 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:688262 HCAPLUS
DN 133:277141
TI Microarrays of ESTs for monitoring multiple gene expression in filamentous fungi
IN Berka, Randy M.; Rey, Michael W.; Shuster, Jeffrey R.; Kauppinen, Sakari; Clausen, Ib Groth; Olsen, Peter Bjarke
PA Novo Nordisk Biotech, Inc., USA; Novo Nordisk A/S
SO PCT Int. Appl., 3161 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000056762	A2	20000928	WO 2000-US7781	20000322

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-273623 19990322
AB The present invention relates to methods for monitoring differential expression of a plurality of genes in a first filamentous fungal cell relative to expression of the same genes in one or more second filamentous fungal cells using microarrays contg. filamentous fungal expressed

sequenced tags. The present invention also relates to filamentous fungal expressed sequenced tags and to computer readable media and substrates contg. such expressed sequenced tags for monitoring expression of a plurality of genes in filamentous fungal cells. DNA sequences are provided for 3770 ESTs from Fusarium venenatum, 606 ESTs from Aspergillus niger, 4024 ESTs from Aspergillus oryzae, and 459 ESTs from Trichoderma reesei.

L138 ANSWER 10 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:646126 HCAPLUS
DN 133:233555
TI Biological substance-containing fiber carriers used for preparing **microarray** or chip
IN Akita, Takashi; Ito, Chiho; Ishimaru, Teruta; Miyauchi, Haruko; Murase, Kei; Takahashi, Atsushi; Umi, Toshinori; Maehara, Osamu; Ikeda, Tadanobu; Oogami, Nobuko; Makino, Takayuki; Yu, Fujio; Watanabe, Fumiaki; Uragaki, Toshitaka; Fujii, Wataru; Morishita, Takeharu
PA Mitsubishi Rayon Co., Ltd., Japan
SO PCT Int. Appl., 129 pp.
CODEN: PIXXD2
DT Patent
LA Japanese
FAN.CNT 2

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000053736	A1	20000914	WO 2000-JP1353	20000306
	W: AE, AU, BA, BG, BR, CA, CN, CZ, HU, ID, IL, IN, KR, MX, NO, NZ, PL, RO, RU, SG, SK, TR, US, YU, ZA				
	RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	JP 2000245460	A2	20000912	JP 1999-59361	19990305
	JP 2000270877	A2	20001003	JP 1999-83964	19990326
	JP 2000270878	A2	20001003	JP 1999-84100	19990326
	JP 2000270879	A2	20001003	JP 1999-84101	19990326
	JP 2000279177	A2	20001010	JP 1999-93043	19990331
	JP 2000342298	A2	20001212	JP 1999-346521	19991206

PRAI JP 1999-59361 19990305
JP 1999-83964 19990326
JP 1999-84100 19990326
JP 1999-84101 19990326
JP 1999-93043 19990331
JP 1999-93044 19990331
JP 1999-215014 19990729
JP 1999-240041 19990826
JP 1999-298613 19991020
JP 1999-324194 19991115
JP 1999-346288 19991206
JP 1999-346309 19991206
JP 1999-346521 19991206
JP 2000-55658 20000301
JP 2000-57075 20000302

AB Fibers (e.g., hollow fiber, porous fiber, porous hollow fiber) carrying immobilized biol. substance (e.g., nucleic acid, amino acid, sugar, lipid), fibers carrying biol. substance-immobilized gel, and fiber alignments contg. bundles of these fibers are described. Slices of these fiber alignments are provided as **microarray** or chip (e.g., DNA **microarray** or DNA chip) for detecting target biol. substances by hybridization. By this method, the immobilized nucleic acid two-dimensional alignment body with a high quantity of immobilized nucleic acid and a **high d**. alignment of nucleic acid mol. species per unit area is manufd. in a large quantity with a low manufg. cost. Diagrams describing the fiber carriers and fiber alignments are given.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File

Anon	1998			WO 9850782 A2	HCAPLUS
Anon	1998			AU 9872872 A	HCAPLUS
Dainakomu KK	1999			JP 11-108928 A	HCAPLUS
Ferguson, J	1996	14	1681	Nat Biotechnol	HCAPLUS
Kyowa Medetsukusu KK	1998			JP 10-179179 A	HCAPLUS
Kyowa Medetsukusu KK	1998			EP 843019 A2	HCAPLUS
Mitsubishi Rayon Co Ltd	1997			JP 09-111010 A	HCAPLUS
Mitsubishi Rayon Co Ltd	1999			JP 11-000959 A	HCAPLUS
Nippon Zeon Co Ltd	1992			JP 04-046193 A	HCAPLUS
Proudnikov, D	1998	259	34	Anal Biochem	HCAPLUS
Teijin Limited	1996			JP 08-188967 A	
Yershov, G	1996	93	4913	Proc Natl Acad Sci U	HCAPLUS
Yuichi, M	1999			JP 11-211694 A	HCAPLUS

L138 ANSWER 11 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:573813 HCAPLUS
DN 133:172992
TI Increasing the efficiency of nucleic acid hybridization by irradiation with ultraviolet to near-infra red light
IN Al-sheikhly, Mohamad; Bentley, William E.; Silverman, Joseph
PA USA
SO PCT Int. Appl., 65 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000047600	A1	20000817	WO 2000-US3357	20000210

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-119417 19990210
US 1999-136185 19990527
AB Photo-induced nucleic acid hybridization is achieved by exposure of a single-stranded nucleic acid mols. to UV (UV), visible (VIS) and near IR (NIR) light. Specifically, irradn. increases the concn. of hydrogen bonded double-strand nucleic acid mols. as a result of complementary base pairing. Hybridization at pH 7.8 is most prevalent using UV (300 nm) irradn., but is detectable even with NIR (920 nm) irradn. Further, the effect is seen at room temp. The results offer promise of practical application in technologies related to **genome arrays**, northern and Southern blotting techniques, PCR, and hybrid nucleic acid-memory devices.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Demers	1998			WO 9812559 A1	HCAPLUS
Heller	1996			US 5565322 A	HCAPLUS
Lacroix	1998			US 5795722 A	HCAPLUS
Macevicz	1991			US 5002867 A	HCAPLUS
McGall	1995			US 5412087 A	HCAPLUS
Pease, A	1994	91	5022	Proc Natl Acad Sci U	HCAPLUS
Yabusaki	1986			US 4599303 A	HCAPLUS
Zehnder	1997	43	1703	Clinical Chemistry	HCAPLUS

L138 ANSWER 12 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:450410 HCAPLUS

TI Monitoring gene expression using DNA **microarrays**
AU Harrington, Christina A.; **Rosenow, Carsten**; Retief, Jacques
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Curr. Opin. Microbiol. (2000), 3(3), 285-291
CODEN: COMIF7; ISSN: 1369-5274
PB Elsevier Science Ltd.
DT Journal
LA English
AB The concurrent development of **high-d. array** technologies and the complete sequencing of a no. of microbial genomes is providing the opportunity to comprehensively and efficiently survey the transcription profile of microorganisms under different conditions and well-defined genotypes. **Microarray**-based studies are uncovering broad patterns of genetic activity, providing new understanding of gene functions and, in some cases, generating unexpected insight into transcriptional processes and biol. mechanisms. One topic that has come to the forefront is how best to effectively manage and interpret the large data sets being generated. Although progress has been made, this remains a challenging opportunity for functional genomics research.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Alon, U	1999	96	6745	Proc Natl Acad Sci U	HCAPLUS
Bassett, D	1999	21	51	Suppl Nat Genet	HCAPLUS
Bowtell, D	1999	21	25	Suppl Nat Genet	HCAPLUS
Brown, P	1999	21	33	Suppl Nat Genet	HCAPLUS
Case-Green, S	1998	2	404	Curr Opin Chem Biol	HCAPLUS
Chambers, J	1999	73	5757	J Virol	HCAPLUS
Chee, M	1996	274	610	Science	HCAPLUS
Cho, R	1998	2	65	Mol Cell, http://gen	HCAPLUS
Chu, S	1998	282	699	Science, http://cmgm	HCAPLUS
Claverie, J	1999	8	1821	Hum Mol Genet	HCAPLUS
De Risi, J	1997	278	680	Science	HCAPLUS
De Saizieu, A	1998	16	45	Nat Biotechnol	HCAPLUS
Duggan, D	1999	21	10	Suppl Nat Genet	HCAPLUS
Eisen, M	1999	303	179	Methods in Enzymolog	HCAPLUS
Eisen, M	1998	95	14863	Proc Natl Acad Sci U	HCAPLUS
Ferea, T	1999	9	715	Curr Opin Genet Dev	HCAPLUS
Ferea, T	1999	96	9721	Proc Natl Acad Sci U	HCAPLUS
Gingeras, T	2000			to be published in A	
Golub, T	1999	286	531	Science	HCAPLUS
Gray, N	1998	281	533	Science	HCAPLUS
Holstege, F	1998	95	717	Cell	HCAPLUS
Jelinsky, S	1999	96	1486	Proc Natl Acad Sci U	HCAPLUS
Lander, E	1999	21	3	Suppl Nat Genet	HCAPLUS
Lashkari, D	1997	94	13057	Proc Natl Acad Sci U	HCAPLUS
Lelivelt, M	1999	19	6710	Mol Cell Biol	HCAPLUS
Lipshutz, R	1999	21	20	Suppl Nat Genet	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Lockhart, D	1998	4	1235	Nat Med	HCAPLUS
Madhani, H	1998	96	12530	Proc Natl Acad Sci U	
Marton, M	1998	4	1293	Nat Med	HCAPLUS
Richmond, C	1999	27	3821	Nucleic Acid Res	HCAPLUS
Schena, M	1996	270	467	Science	
Spellman, P	1998	9	3273	Mol Biol Cell, http:	HCAPLUS
Tamayo, P	1999	96	2907	Proc Natl Acad Sci U	HCAPLUS
Tao, H	1999	181	6425	J Bacteriol	HCAPLUS
Tavazoie, S	1999	22	281	Nat Genet	HCAPLUS
Toronen, P	1999	451	142	FEBS Lett	HCAPLUS
Wilson, M	1999	96	12833	Proc Natl Acad Sci U	HCAPLUS
Winzeler, E	1999	306	3	Methods in Enzymolog	HCAPLUS
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS
Zhu, H	1998	95	14470	Proc Natl Acad Sci	HCAPLUS

L138 ANSWER 13 OF 67 HCAPLUS COPYRIGHT 2001 ACS

AN 2000:441968 HCAPLUS
DN 133:69783
TI High throughput assay system for monitoring ESTs using ordered **arrays** of probes
IN Felder, Stephen; Seligmann, Bruce; Kris, Richard M.
PA USA
SO PCT Int. Appl., 88 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000037683	A2	20000629	WO 1999-US30492	19991222

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1998-218089 19981222
AB The present invention relates to compns., app. and methods useful for concurrently performing multiple, high throughput, biol. or chem. assays, using repeated **arrays** of probes. A combination of the invention comprises a surface, which comprises a plurality of test regions, at least two of which, and in a preferred embodiment, at least twenty of which, are substantially identical, wherein each of the test regions comprises an **array** of generic anchor mols. The anchors are assocd. with bifunctional linker mols., each contg. a portion which is specific for at least one of the anchors and a portion which is a probe specific for a target of interest. The resulting **array** of probes is used to analyze the presence or test the activity of one or more target mols. which specifically interact with the probes. In one embodiment of the invention, the test regions (which can be wells) are further subdivided into smaller subregions (indentations, or dimples). In one embodiment of the invention, ESTs are mapped. In another embodiment, the presence of a target nucleic acid is detected by protecting the target against nuclease digestion with a polynucleotide fragment, and analyzing the protected polynucleotide by mass spectrometry.

L138 ANSWER 14 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:441816 HCAPLUS
DN 133:69835
TI Complementary DNAs encoding human proteins with signal peptides
IN Bougueleret, Lydie; Dumas, Jean-Baptiste; Duclert, Aymeric
PA Genset, Fr.
SO PCT Int. Appl., 306 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 4

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000037491	A2	20000629	WO 1999-IB2058	19991220

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

WO 2001000803 A2 20010104 WO 2000-IB1011 20000621
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 1998-113686 19981222
US 1999-141032 19990625
WO 1999-IB2058 19991220
US 1999-469099 19991221
AB The sequences of 50 cDNAs encoding secreted proteins are disclosed. Four of these secreted proteins are closely related to known proteins: human parotid secretory protein HPSP, a human transmembrane protein, murine putative sialyltransferase protein, and murine recombination activating gene 1 inducing protein. The cDNAs can be used to express secreted proteins or fragments thereof or to obtain antibodies capable of specifically binding to the secreted proteins. Signal peptide-contg. proteins are expected to have biol. activities (no data). The cDNAs may also be used in diagnostic, forensic, gene therapy, and chromosome mapping procedures. The cDNAs may also be used to design expression vectors and secretion vectors.

L138 ANSWER 15 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:314871 HCAPLUS
DN 132:330583
TI Nucleic acid analysis using sequence-targeted tandem stacking hybridization of pre-annealed duplex probes
IN Beattie, Kenneth Loren; Maldonado Rodriguez, Rogelio
PA USA
SO PCT Int. Appl., 129 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000026412	A1	20000511	WO 1999-US25693	19991102

W: CA, JP, MX
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRAI US 1998-106655 19981102
AB The disclosed invention provides a novel method for analyzing **genomic** DNA and expressed sequences, using auxiliary oligonucleotides preannealed to the single-stranded target nucleic acid to form a partially duplex target mol., which offers several advantages in the anal. of nucleic acid sequences by hybridization to genosensor **arrays** or "DNA chips". Also provided is a method for directly analyzing and comparing patterns of gene expression at the level of transcription in different cellular samples.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Birkenmeyer	1995			US 5427930 A	HCAPLUS
Cantor	1996			US 5503980 A	HCAPLUS
Dellinger	1998			US 5853993 A	HCAPLUS
Lane	1998			US 5770365 A	HCAPLUS
Muller	1998			US 5804384 A	HCAPLUS
Picone	1996			US 5491225 A	HCAPLUS
Picone	1997			US 5614388 A	HCAPLUS
Tyagi	1998			US 5759773 A	HCAPLUS
Tyagi	1999			US 5925517 A	HCAPLUS

L138 ANSWER 16 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:291302 HCAPLUS
DN 132:318582
TI Tissue **arrays** and methods of detecting and using genetic disorders
IN Kallioniemi, Olli-p; Muller, Uwe Richard; Sauter, Giudo; Kononen, Juha; Barlund, Maarit
PA Vysis, Inc., USA; United States Dept. of Health and Human Services
SO PCT Int. Appl., 87 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000024940	A1	20000504	WO 1999-US25370	19991028
W: CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
PRAI US 1998-106038		19981028		
US 1999-150493		19990824		

AB A method is disclosed for rapid mol. profiling of tissue or other cellular specimens by placing a donor specimen in an assigned location in a recipient **array**, providing copies of the **array**, and performing a different biol. anal. of each copy. The results of the different biol. analyses are compared to det. if there are correlations between the results of the different biol. analyses at each assigned location. In some embodiment, the specimens may be tissue specimens from different tumors, which are subjected to multiple parallel mol. (including genetic and immunol.) analyses. The results of the parallel analyses are then used to detect common mol. characteristics of the genetic disorder type, which can subsequently be used in the diagnosis or treatment of the disease. The biol. characteristics of the tissue can be correlated with clin. or other information, to detect characteristics assocd. with the tissue, such as susceptibility or resistance to particular types of drug treatment. Other examples of suitable tissues which can be placed in the matrix include tissue from transgenic or model organisms, or cellular suspensions (such as cytol. prepns. or specimens of liq. malignancies or cell lines). Thus, characteristics of various cancers, e.g., breast, prostate, renal cell carcinoma, were detd. using tissue **arrays** for immunohistochem. anal., comparative **genome** hybridization anal., etc.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Forozan, F	1997	13	405	Trends in Genetics	HCAPLUS
Joos, S	1995	14	267	Genes Chromosomes an	HCAPLUS
Pinkel	1997			US 5665549 A	HCAPLUS
Pinkel	1997			US 5690894 A	HCAPLUS
Pinkel	1999			US 5976790 A	HCAPLUS
Pinkel, D	1998	20	207	Nature Genetics	HCAPLUS

L138 ANSWER 17 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:291301 HCAPLUS
DN 132:330597
TI Methods of lowering sequence complexity in the analysis of **genomic** DNA
IN Dong, Shoulian; Lipshutz, Robert J.; Lockhart, David J.
PA Affymetrix, Inc., USA
SO PCT Int. Appl., 75 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000024939	A1	20000504	WO 1999-US25200	19991027

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1998-105867 19981027
US 1999-136125 19990526

AB The present invention provides for novel methods of sample prepn. and anal. involving reproducibly reducing the complexity of a nucleic sample such as a **genomic** DNA. The invention further provides for anal. of the above sample by hybridization to an **array** which may be specifically designed to interrogate the desired fragments for particular characteristics, such as, for example, the presence or absence of a polymorphism. The invention further provides for novel methods of using a computer system to model enzymic reactions in order to det. exptl. conditions before conducting actual expts. One method of lowering complexity is to use type IIS restriction enzymes to create digests with nos. of different sticky ends and then ligate these with a family of adaptor mols. with a common core that can be used for PCR amplification and different 3'-ends. Another approach is the use of arbitrarily-primed PCR to create a sub-population of the total **genomic** DNA.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Rothberg	1999			US 5972693 A	HCAPLUS

L138 ANSWER 18 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:263592 HCAPLUS
DN 134:66728
TI Large-scale **genomic** analysis using Affymetrix **GeneChip** probe **arrays**
AU Warrington, Janet A.; Dee, Suzanne; Trulson, Mark
CS Affymetrix, Inc., Santa Clara, CA, USA
SO Microarray Biochip Technol. (2000), 119-148. Editor(s): Schena, Mark. Publisher: Eaton Publishing Co., Natick, Mass.
CODEN: 68VMAZ
DT Conference; General Review
LA English
AB A review with 50 refs. of the **GeneChip**.RTM. system from Affymetrix. Topics include: a brief overview of the characteristics of the technol. that distinguish it from other DNA **microarray** hybridization technologies; an introduction to **array** design, probe selection, and **array** synthesis; a description of current applications including results from recent expts.; and a brief discussion on future applications.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Beecher, J	1997	76	597	Polymeric Mater Sci	HCAPLUS
Canman, C	1998	17	3301	Oncogene	
Chee, M	1996	274	610	Science	HCAPLUS
Cho, R	1998	95	3752	Proc Natl Acad Sci U	HCAPLUS
Condra, J	1998	4	610	Haemophilia	MEDLINE
Cronin, M	1996	7	244	Hum Mutat	HCAPLUS
DeRisi, J	1997	278	680	Science	HCAPLUS
de Saizieu, A	1998	16	45	Nat Biotechnol	HCAPLUS
Der, S	1998	95	15623	Proc Natl Acad Sci U	HCAPLUS

Eichelbaum, M	1996	23	983	Clin Exp Pharmacol P	HCAPLUS
Erickson, J	1996	36	545	Annu Rev Pharmacol T	HCAPLUS
Fodor, S	1991	251	713	Science	
Fodor, S	1993	364	555	Science	MEDLINE
Giaever, G	1999	21	278	Nat Genet	HCAPLUS
Gingeras, T	1998	8	435	Genome Res	HCAPLUS
Gunderson, K	1998	8	1142	Genome Res	HCAPLUS
Gunthard, H	1998	14	869	AIDS Res Hum Retrovi	HCAPLUS
Hacia, J	1998	8	1245	Genome Res	HCAPLUS
Hacia, J	1996	14	441	Nat Genet	HCAPLUS
Hammer, S	1997	337	725	N Engl J Med	HCAPLUS
Havlir, D	1998	12	S165	AIDS	
Hollstein, M	1991	253	49	Science	HCAPLUS
Holstege, F	1998	95	717	Cell	HCAPLUS
Ingelman-Sundberg, M	1998	102-1	155	Toxicol Lett	HCAPLUS
Jelinsky, S	1999	96	1486	Genetics	HCAPLUS
Kozal, M	1996	2	753	Nat Med	HCAPLUS
Levine, A	1997	88	323	Cell	HCAPLUS
Liu, W	1997	61	1494	Am J Hum Genet	
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Mahadevappa, M	1999	17	1134	Nat Biotechnol	HCAPLUS
McGall, G	1996	93	13555	Proc Natl Acad Sci U	HCAPLUS
Mellentin, J	1989	58	77	Cell	HCAPLUS
Meyer, U	1997	37	269	Annu Rev Pharmacol T	HCAPLUS
Meyer, U	1996	24	449	J Pharmacokinet Biop	HCAPLUS
Miki, Y	1994	266	66	Science	HCAPLUS
Miller, M	1997	40	1	Fundam Appl Toxicol	HCAPLUS
Platzer, M	1997	7	592	Genome Res	HCAPLUS
Redfern, C				Cell in press	
Rotman, G	1997	29	285	Cancer Surv	HCAPLUS
Sapolsky, R	1996	33	445	Genomics	HCAPLUS
Shafer, R	1999	27	348	Nucleic Acids Res	HCAPLUS
Shoemaker, D	1996	14	450	Nat Genet	HCAPLUS
Sturniolo, T	1999			Nat Biotechnol in pr	
Touw, D	1997	14	55	Drug Metabol Drug In	HCAPLUS
Troesch, A	1999	37	49	J Clin Microbiol	HCAPLUS
Wang, D	1998	280	1077	Science	HCAPLUS
Warrington, J	1997	61	A36	Am J Hum Genet Suppl	
Winzeler, E	1998	281	1194	Science	HCAPLUS
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS
Zhu, H	1998	95	14470	Microbiology	HCAPLUS

L138 ANSWER 19 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:260598 HCAPLUS
DN 132:275155
TI Quantitative analysis of hybridization patterns and intensities in oligonucleotide **arrays** for detecting mutation and gene expression
IN Levine, Arnold J.; Alon, Uri
PA Princeton University, USA
SO PCT Int. Appl., 28 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000022173	A1	20000420	WO 1999-US24388	19991014

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,

CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 1998-174364 19981015
AB Systems and methods for enhanced quant. anal. of hybridization intensity measurements obtained from oligonucleotide probes and other probes exposed to target samples are provided by virtue of the present invention. One embodiment ameliorates the effects of high frequency noise superimposed on a hybridization intensity measurement signal measured over successive probe alignments to a target sample sequence. Detection of expressed genes and ESTs and quant. measurement of expression level may be improved. Mutation detection and base calling may be improved.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Brenner	1997			US 5695934 A	HCAPLUS
Chee	1998			US 5795716 A	HCAPLUS
Fodor	1998			US 5800992 A	HCAPLUS
Hollis	1997			US 5653939 A	HCAPLUS
Isis Innovation Limited	1989		5	WO 8910977 A1	HCAPLUS
Southern	1997			US 5700637 A	HCAPLUS

L138 ANSWER 20 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:244036 HCAPLUS
DN 132:247049
TI Large-scale discovery and genotyping of single-nucleotide polymorphisms in the mouse
AU Lindblad-Toh, Kerstin; Winchester, Ellen; Daly, Mark J.; Wang, David G.; Hirschhorn, Joel N.; Laviolette, Jean-Philippe; Ardlie, Kristin; Reich, David E.; Robinson, Elizabeth; Sklar, Pamela; Shah, Nila; Thomas, Daryl; Fan, Jian-Bing; **Gingeras, Thomas**; Warrington, Janet; Patil, Nila; Hudson, Thomas J.; Lander, Eric S.
CS Whitehead Institute/MIT Center for Genome Research, Whitehead Institute for Biomedical Research, Cambridge, MA, USA
SO Nat. Genet. (2000), 24(4), 381-386
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal
LA English
AB Single-nucleotide polymorphisms (SNPs) have been the focus of much attention in human genetics because they are extremely abundant and well-suited for automated large-scale genotyping. Human SNPs, however, are less informative than other types of genetic markers (such as simple-sequence length polymorphisms or microsatellites) and thus more loci are required for mapping traits. SNPs offer similar advantages for exptl. genetic organisms such as the mouse, but they entail no loss of informativeness because bi-allelic markers are fully informative in analyzing crosses between inbred strains. A large-scale anal. of SNPs in the mouse genome is reported. The rate of nucleotide polymorphism was characterized in 8 mouse strains and a collection of 2848 SNPs located in 1755 sequence-tagged sites (STSs) identified using **high-d.** oligonucleotide **arrays**. Three-quarters of these SNPs have been mapped on the mouse genome, providing a first-generation SNP map of the mouse. Also, a multiplex genotyping procedure was developed by which a genome scan can be performed with only 6 genotyping reactions per animal.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Atchley, W	1993	10	1150	Mol Biol Evol	MEDLINE
Beck, J	2000	24	23	Nature Genet	HCAPLUS
Cargill, M	1999	22	231	Nature Genet	HCAPLUS
Chee, M	1996	274	610	Science	HCAPLUS
Dietrich, W	1996	380	149	Nature	HCAPLUS
Ferris, K	1983	105	681	Genetics	
Nusbaum, C	1999	22	388	Nature Genet	HCAPLUS

Sage, R	1981		40	The Mouse in Biomedi	
Syvanen, A	1999	13	1	Hum Mutat	HCAPLUS
Van Etten, W	1999	22	384	Nature Genet	HCAPLUS
Wang, D	1998	280	1077	Science	HCAPLUS

L138 ANSWER 21 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:220713 HCAPLUS
DN 132:247134
TI Optimization of hybridization media for hybridization assays using oligonucleotides **arrays**.
IN Cronin, Maureen T.; Miyada, Charles Garrett; Trulson, Mark; **Gingeras, Thomas R.**; McGall, Glenn; Robinson, Claire; Oval, Michelle
PA Affymetrix, Inc., USA
SO U.S., 11 pp., Cont.-in-part of U.S. Ser. No. 544,381.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 7

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6045996	A	20000404	US 1996-648709	19960516
WO 9511995	A1	19950504	WO 1994-US12305	19941026
W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ				
RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
US 5837832	A	19981117	US 1995-441887	19950516
US 6027880	A	20000222	US 1995-544381	19951010
US 5861242	A	19990119	US 1997-781550	19970109
WO 9743450	A1	19971120	WO 1997-US8446	19970516
W: AU, CA, JP, US				
RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9730090	A1	19971205	AU 1997-30090	19970516

PRAI	US 1993-143312	19931026
	US 1994-284064	19940802
	WO 1994-US12305	19941026
	US 1995-510521	19950802
	US 1995-544381	19951010
	US 1993-82937	19930625
	US 1996-648709	19960516
	WO 1997-US8446	19970516

AB This invention provides methods of performing nucleic acid hybridization assays on **high-d.** substrate-bound oligonucleotide **arrays** involving including in the hybridization mixt. an isostabilizing agent, a denaturing agent or a renaturation accelerant. The use of betaine 4-6M as an isostabilizing agent is demonstrated in reconstruction expts. that discriminated between test samples showing small nos. of single base changes.

L138 ANSWER 22 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:145067 HCAPLUS
DN 132:206569
TI Expression monitoring for human cytomegalovirus (HCMV) infection, and genes possibly involved in mediating the pathology of HCMV infection
IN Zhu, Hua; **Gingeras, Thomas**; Shenk, Thomas
PA Affymetrix, Inc., USA
SO PCT Int. Appl., 69 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI WO 2000011218 A1 20000302 WO 1999-US18772 19990820
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9956776 A1 20000314 AU 1999-56776 19990820
PRAI US 1998-97708 19980821
WO 1999-US18772 19990820
AB The invention provides methods, compns., and app. for studying the complex regulatory relationships among host genes and viruses, in particular HCMV. The invention also provides cellular mRNAs whose levels change by a factor of four or more after infection with HCMV. Such genes are likely those involved in mediating the pathol. of the infected tissues. Thus by identifying agents which are able to reverse the induction or repression of such genes, one can find candidate therapeutic agents for use in treating and or preventing HCMV-caused disease pathologies.

L138 ANSWER 23 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:138517 HCAPLUS
DN 132:330384
TI **Microarray** technology - enhanced versatility, persistent challenge
AU Epstein, Charles B.; Butow, Ronald A.
CS Department of Molecular Biology, University of Texas Southwestern Medical Center, Dallas, TX, 75390-9148, USA
SO Curr. Opin. Biotechnol. (2000), 11(1), 36-41
CODEN: CUOBE3; ISSN: 0958-1669
PB Current Biology Publications
DT Journal; General Review
LA English
AB A review with refs. **Microarray** anal. of nucleic acid related phenomena on a **genome**-wide scale is now a proven technol. New applications of the method are appearing rapidly and problems unique to the handling and interpretation of the large data sets produced by the technique are beginning to be addressed.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Alon, U	1999	96	6745	Proc Natl Acad Sci U	HCAPLUS
Amundson, S	1999	18	3666	Oncogene	HCAPLUS
Anon				http://cmgm.stanford	
Anon				http://cmgm.stanford	
Bassett, D	1999	21	51	Nat Genet	HCAPLUS
Behr, M	1999	284	1520	Science	HCAPLUS
Bowtell, D	1999	21	25	Nat Genet	HCAPLUS
Braxton, S	1998	9	643	Curr Opin Biotechnol	HCAPLUS
Bryant, Z	1999	96	5559	Proc Natl Acad Sci U	HCAPLUS
Cargill, M	1999	22	231	Nat Genet	HCAPLUS
Chen, Y	1997	2	364	J Biomedical Optics	HCAPLUS
Cho, R	1998	2	65	Mol Cell	HCAPLUS
Chu, S	1998	282	699	Science	HCAPLUS
Diatchenko, L	1999	303	349	Methods Enzymol	HCAPLUS
Eisen, B	1998	95	14863	Proc Natl Acad Sci U	
Eisen, M	1999	303	179	Methods Enzymol	HCAPLUS
Fambrough, D	1999	97	727	Cell	HCAPLUS
Ferea, T	1999	96	9721	Proc Natl Acad Sci U	HCAPLUS
Galitski, T	1999	285	251	Science	HCAPLUS
Geschwind, D	1998	23	215	Dev Genet	HCAPLUS
Hacia, J	1999	22	164	Nat Genet	HCAPLUS
Hilsenbeck, S	1999	91	453	J Natl Cancer Inst	MEDLINE

Holstege, F	1998	95	717	Cell	HCAPLUS
Iyer, V	1999	283	83	Science	HCAPLUS
Jelinsky, S	1999	96	1486	Proc Natl Acad Sci U	HCAPLUS
Kallioniemi, A	1992	258	818	Science	HCAPLUS
Khan, J	1998	58	5009	Cancer Res	HCAPLUS
Lee, C	1999	285	1390	Science	HCAPLUS
Lipshutz, R	1999	21	20	Nat Genet	HCAPLUS
Lisitsyn, N	1993	259	946	Science	HCAPLUS
Marton, M	1998	4	1293	Nat Med	HCAPLUS
Norman, T	1999	285	591	Science	HCAPLUS
Perou, C	1999	96	9212	Proc Natl Acad Sci U	HCAPLUS
Pinkel, D	1998	20	207	Nat Genet	HCAPLUS
Pollack, J	1999	23	41	Nat Genet	HCAPLUS
Schena, M	1999			DNA Microarrays - a	
Sinclair, B	1999	17	18	The Scientist	
Singh-Gasson, S	1999	17	974	Nat Biotechnol	HCAPLUS
Solinas-Toldo, S	1997	20	399	Genes Chromosomes Ca	HCAPLUS
Somerville, C	1999	285	380	Science	HCAPLUS
Spellman, P	1998	9	3273	Mol Biol Cell	HCAPLUS
Tamayo, P	1999	96	2907	Proc Natl Acad Sci U	HCAPLUS
Tavazoie, S	1999	22	281	Nat Genet	HCAPLUS
The Chipping Forecast	1999	21	1	Nat Genet	
Toronen, P	1999	451	142	FEBS Lett	HCAPLUS
Wang, K	1999	229	101	Gene	HCAPLUS
Watson, A	1998	9	609	Curr Opin Biotechnol	HCAPLUS
Welford, S	1998	26	3059	Nucleic Acids Res	HCAPLUS
Wittes, J	1999	91	400	J Natl Cancer Inst	MEDLINE
Yang, G	1999	27	1517	Nucleic Acids Res	HCAPLUS

L138 ANSWER 24 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:53947 HCAPLUS
DN 132:103733
TI Methods for determining cross-hybridization based on dissociation kinetics
IN Burchard, Julja; Stoughton, Roland; Friend, Stephen H.
PA Rosetta Inpharmatics, Inc., USA
SO PCT Int. Appl., 72 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2000003039	A1	20000120	WO 1999-US15813	19990713
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US 6171794	B1	20010109	US 1999-335971	19990618
AU 9950992	A1	20000201	AU 1999-50992	19990713

PRAI US 1998-92512 19980713
US 1999-335971 19990618
WO 1999-US15813 19990713

AB The present invention provides methods for distinguishing the fractions of polynucleotide sequences which hybridize to any given probe, including probes on **microarrays** such as those described herein. In particular, the present invention enables users to identify the fraction of sequences which are perfectly complementary to a probe, thereby correcting for effects of cross-hybridization in a hybridization assay. The methods of the invention work by monitoring the kinetics of dissocn. of sequences from the probe so that a resulting "dissocn. curve" may be compared to a combination of the individual "dissocn. profiles" for each

sequence which hybridizes. In alternative embodiments, the invention also provides computer systems for performing the present methods, as well as databases of the dissocn. profiles.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Affymetrix Inc	1998			WO 9812354 A1	HCAPLUS
Blake, R	1995		207	Denaturation of DNA	
Ikuta	1987	15	797	Nuc Aci Res	HCAPLUS
Stimpson	1997			US 5599668 A	HCAPLUS
Stimpson	1995	92	6379	Proc Natl Acad Sci U	HCAPLUS
Wetmur, J	1995		605	Nucleic Acid Hybrids	

L138 ANSWER 25 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:41290 HCAPLUS
DN 132:190171
TI High throughput analysis of gene expression in the human brain
AU Colantuoni, Carlo; Purcell, Amy E.; Bouton, Christopher M. L.; Pevsner, Jonathan
CS Department of Neurology, Kennedy Krieger Research Institute, Baltimore, MD, 21205, USA
SO J. Neurosci. Res. (2000), 59(1), 1-10
CODEN: JNREDK; ISSN: 0360-4012
PB Wiley-Liss, Inc.
DT Journal; General Review
LA English
AB A review with > 100 refs. The human brain is thought to have the greatest complexity of gene expression of any region of the body, reflecting the diverse functions of neurons and glia. Studies of gene expression in the human brain may yield fundamental information about the phenotype of brain cells in different stages of development, in different brain regions, and in different physiol. and pathol. states. As the human **genome** project nears completion, several technol. advances allow the anal. of thousands of expressed genes in a small brain sample. This review describes available sources of human brain material, and several high throughput techniques used to measure the expression of thousands of genes. These techniques include expressed sequence tag (EST) sequencing of cDNA libraries; differential display; subtractive hybridization; serial anal. of gene expression (SAGE); and the emerging technol. of **high d.** DNA **microarrays**. Measurement of gene expression with **microarrays** and other technologies has potential applications in the study of human brain diseases, including cognitive disorders for which animal models are typically not available. Gene expression measurements may be used to identify genes that are abnormally regulated as a secondary consequence of a disease state, or to identify the response of brain cells to pharmacol. treatments.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Abrams, M	1999	82	25	Am J Med Genet	MEDLINE
Adams, M	1993	4	256	Nat Genet	HCAPLUS
Adams, M	1993	4	373	Nat Genet	HCAPLUS
Adams, M	1992	355	632	Nature	HCAPLUS
Adams, M	1991	252	1651	Science	HCAPLUS
Alon, U	1999	96	6745	Proc Natl Acad Sci U	HCAPLUS
Audic, S	1997	7	986	Genome Res	HCAPLUS
Barton, A	1993	61	1	J Neurochem	HCAPLUS
Bell, J	1997	23	281	Neuropathol Appl Neu	MEDLINE
Bernal, J	1990	27	153	J Neurosci Res	HCAPLUS
Bolay, H	1996	98	305	Clin Neurol Neurosur	MEDLINE
Bonaldo, M	1996	6	791	Genome Res	HCAPLUS
Bowtell, D	1999	21	25	Nat Genet	MEDLINE
Brown, P	1999	21	33	Nat Genet	MEDLINE
Carulli, J	1998	30-31	286	J Cell Biochem Suppl	MEDLINE

Cirelli, C	1999	8	44	J Sleep Res	
Comincini, S	1999	19	277	Anticancer Res	HCAPLUS
Cossman, J	1999	94	411	Blood	HCAPLUS
Crino, P	1996	93	14152	Proc Natl Acad Sci U	HCAPLUS
DeRisi, J	1996	14	457	Nat Genet	HCAPLUS
Diatchenko, L	1996	93	6025	Proc Natl Acad Sci U	HCAPLUS
Drmanac, S	1996	37	29	Genomics	HCAPLUS
Dron, M	1996	2	240	J Neurovirol	HCAPLUS
Duggan, D	1999	21	10	Nat Genet	MEDLINE
Eisen, M	1998	95	14863	Proc Natl Acad Sci U	HCAPLUS
Emmert-Buck, M	1996	274	998	Science	HCAPLUS
Ensoli, F	1998	86	881	Neuroscience	HCAPLUS
Ermolaeva, O	1998	20	19	Nat Genet	HCAPLUS
Fan, L	1999	23	408	Alcohol Clin Exp Res	HCAPLUS
Fung, B	1991	11	701	J Neurosci	HCAPLUS
Gautvik, K	1996	93	8733	Proc Natl Acad Sci U	HCAPLUS
Ginsberg, S	1999	45	174	Ann Neurol	MEDLINE
Gygi, S	1999	19	1720	Mol Cell Biol	HCAPLUS
Hacia, J	1996	14	441	Nat Genet	HCAPLUS
Hahn, W	1971	173	158	Science	HCAPLUS
Harrison, P	1995	200	151	Neurosci Lett	HCAPLUS
Heller, R	1997	94	2150	Proc Natl Acad Sci U	HCAPLUS
Hutchins, G	1994	118	19	Arch Pathol Lab Med	MEDLINE
Iyer, V	1999	283	83	Science	HCAPLUS
Johnson, G	1994	15	675	Neurobiol Aging	MEDLINE
Johnston, N	1997	77	83	J Neurosci Methods	HCAPLUS
Kacharmina, J	1999	303	3	Methods Enzymol	HCAPLUS
Khan, J	1999	1423	M17	Biochem Biophys Acta	HCAPLUS
Kito, K	1997	184	73	Gene	HCAPLUS
Kobayashi, H	1990	2	29	J Mol Neurosci	HCAPLUS
Kristensson, K	1992	16	45	Mol Chem Neuropathol	MEDLINE
Kukekov, V	1999	156	333	Exp Neurol	HCAPLUS
Labudova, O	1999	96	279	Clin Sci (Colch)	HCAPLUS
Labudova, O	1999	64	1037	Life Sci	HCAPLUS
Larsen, S	1992	100	498	APMIS	HCAPLUS
Lashkari, D	1997	94	13057	Proc Natl Acad Sci U	HCAPLUS
Leonard, S	1993	33	456	Biol Psychiatry	HCAPLUS
Liang, S	1998	3	18	Pac Symp Biocomput	
Ligon, A	1998	4	217	Neurovirol	MEDLINE
Ligtenberg, M	1995	56	44	Am J Hum Genet	HCAPLUS
Lipshutz, R	1999	21	20	Nat Genet	MEDLINE
Lisitsyn, N	1993	259	946	Science	HCAPLUS
Livesey, F	1996	19	84	Trends Neurosci	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Maniotis, A	1999	155	739	Am J Pathol	MEDLINE
Marra, M	1999	21	191	Nat Genet	HCAPLUS
Michaels, G	1998	3	42	Pac Symp Biocomput	
Miller, F	1987	7	2433	J Neurosci	HCAPLUS
Milner, R	1983	11	5497	Nucleic Acids Res	HCAPLUS
O'Hara, B	1999	19	3781	J Neurosci	HCAPLUS
O'Neill, M	1997	25	2681	Nucleic Acids Res	HCAPLUS
Petito, C	1995	146	1121	Am J Pathol	MEDLINE
Rapin, I	1998	43	7	Ann Neurol	MEDLINE
Ravid, R	1992	93	83	Prog Brain Res	HCAPLUS
Rhee, C	1999	18	2711	Oncogene	HCAPLUS
Roberts, J	1994	100	33	Prog Brain Res	MEDLINE
Ronnett, G	1994	63	1081	Neuroscience	HCAPLUS
Sagerstrom, C	1997	66	751	Annu Rev Biochem	HCAPLUS
Sainz, J	1993	39	135	J Neural Transm Supp	MEDLINE
Sanders, V	1996	2	249	J Neurovirol	HCAPLUS
Santiard-Baron, D	1999	158	206	Exp Neurol	HCAPLUS
Schena, M	1995	270	467	Science	HCAPLUS
Schramm, M	1999	106	329	J Neural Transm	HCAPLUS
Sehgal, A	1998	76	451	Int J Cancer	MEDLINE
Sehgal, A	1998	67	234	J Surg Oncol	MEDLINE
Shapshak, P	1986	16	281	J Neurosci Res	MEDLINE

Somogyi, R	1996	1	45	Complexity	
Somogyi, R	1999	25	834	Soc Neurosci Abstr	
Spellman, P	1998	9	3273	Mol Biol Cell	HCAPLUS
Strachan, T	1997	16	126	Nat Genet	HCAPLUS
Takahashi, N	1995	164	219	Gene	HCAPLUS
Takahashi, Y	1992	38	523	Prog Neurobiol	HCAPLUS
Takeshima, H	1994	80	1056	J Neurosurg	HCAPLUS
Uchiyama, C	1995	37	464	Neurosurgery	MEDLINE
Usui, H	1994	14	4915	J Neurosci	HCAPLUS
Velculescu, V	1995	270	484	Science	HCAPLUS
Vietor, I	1997	1359	187	Biochim Biophys Acta	HCAPLUS
Vingron, M	1999	77	3	J Mol Med	MEDLINE
Walker, M	1999		282	Proceedings of the S	MEDLINE
Wan, J	1996	14	1685	Nature Biotechnol	HCAPLUS
Wang, K	1999	229	101	Gene	HCAPLUS
Watson, J	1993	15	77	Dev Neurosci	HCAPLUS
Wen, X	1998	95	334	Proc Natl Acad Sci U	HCAPLUS
Whitney, L	1999	46	425	Ann Neurol	HCAPLUS
Woychik, R	1998	400	3	Mutat Res	HCAPLUS
Zhang, L	1997	276	1268	Science	HCAPLUS
Zhao, N	1995	156	207	Gene	HCAPLUS

L138 ANSWER 26 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 2000:31285 HCAPLUS
DN 132:89214
TI Nucleic acid affinity columns
IN Lipshutz, Robert J.; Morris, Macdonald S.; Chee, Mark S.; **Gingeras, Thomas R.**
PA Affymetrix, Inc., USA
SO U.S., 16 pp.
CODEN: USXXAM
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 6013440	A	20000111	US 1997-815395	19970310
PRAI US 1996-13231		19960311		

AB This invention provides nucleic acid affinity matrixes that bear a large no. of different nucleic acid affinity ligands allowing the simultaneous selection and removal of a large no. of preselected nucleic acids from the sample. Methods of producing such affinity matrixes are also provided. In general the methods involve the steps of (a) providing a nucleic acid amplification template **array** comprising a surface to which are attached at least 50 oligonucleotides having different nucleic acid sequences, and wherein each different oligonucleotide is localized in a predetd. region of said surface, the d. of said oligonucleotides is greater than about 60 different oligonucleotides per 1 cm2, and all of said different oligonucleotides have an identical terminal 3' nucleic acid sequence and an identical terminal 5' nucleic acid sequence. (b) amplifying said multiplicity of oligonucleotides to provide a pool of amplified nucleic acids; and (c) attaching the pool of nucleic acids to a solid support.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Anon	1988			WO 8801302	HCAPLUS
Anon	1988			WO 8810977	
Anon	1990			EP 0392546	HCAPLUS
Anon	1990			WO 9003382	HCAPLUS
Anon	1993			WO 9317126	HCAPLUS
Anon	1996			EP 0717113	HCAPLUS
Anon	1997			WO 9710365	HCAPLUS
Anon	1994	22		Nucleic Acids Resear	
Dower	1996			US 5547839	HCAPLUS

Drmanac	1993			US 5202231	HCAPLUS
Duncan, C	1988	165	104	Analytical Biochemis	
Holmes	1996			US 5527681	HCAPLUS
Meinkoth, J	1984	138	267	Analytical Biochemis	HCAPLUS
Pirrung	1992			US 5143854	HCAPLUS
Utermohlen	1995			US 5437976	HCAPLUS

L138 ANSWER 27 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:819528 HCAPLUS
DN 132:60101
TI A large-scale automated method for detecting, analyzing, and mapping RNA transcripts
IN Leary, Jeffrey J.; Tal-singer, Ruth
PA Smithkline Beecham Corp., USA
SO PCT Int. Appl., 54 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9967422	A1	19991229	WO 1999-US13813	19990618

W: CA, JP, US
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRAI US 1998-90464 19980624
AB A genetic anal. method termed "fine **array** transcript mapping" or "FAT Mapping" that can be used for transcript mapping of large **genomes** is described. The method can be used to explore differential expression of a template **genome**, and for accurately mapping the 5' ends of transcripts. Further, the presence or absence in any particular biol. circumstances of a given transcript and its relative concn. can define gene functions or coding capacities. Thus the method relates to mapping and identifying novel and known gene products and investigating gene functions and regulation. The method uses large, **high-d.** ordered **arrays** of overlapping clones as the target. Algorithmic anal. of hybridization patterns can be used to identify genes transcribed in a given sample. The method is demonstrated by using it to map gene expression by herpes simplex virus 2 during its life cycle. FAT mapping can also be used to identify the stage in the virus life cycle at which an antiviral agent acts and its mode of action.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Chee	1998			US 5837832 A	HCAPLUS
Daly	1991			US 5019506 A	HCAPLUS
Drmanac	1996			US 5525464 A	HCAPLUS
Schena, M	1996	18	427	BioEssays	HCAPLUS
Tsou	1998	50	331	Genomics	HCAPLUS
Velicer	1992			US 5138033 A	HCAPLUS

L138 ANSWER 28 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:708928 HCAPLUS
DN 131:332950
TI Function-based gene discovery using unique oligonucleotide-tagged bar-coded vectors for clone tracking and automation in cDNA library screening
IN Cen, Hui; Sun, Shaojian
PA Genova Pharmaceuticals Corporation, USA
SO PCT Int. Appl., 68 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

PI WO 9955886 A1 19991104 WO 1999-US8823 19990421
W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
AU 9935727 A1 19991116 AU 1999-35727 19990421
PRAI US 1998-65775 19980424
WO 1999-US8823 19990421

AB The present invention relates generally to the field of **genomics**. More particularly, the present invention relates to methods for function-based gene discovery. Genes are identified as having or being assocd. with a specific function, as participating in a specific functional pathway, or as being a member of a specific functional group, by functional expression in one or more biol. readout assays. This invention is based, at least in part, on the recognition that the signal-to-noise ratio of a readout assay used to screen a cDNA library can be significantly enhanced by methods which localize multiple mol. copies of each unique clone into discrete regions or compartments prior to functional expression. In one embodiment, this invention provides methods for in situ transfection of a sorted library in a "bar-coded" vector to carry out expression of genes from libraries being screened in readout cells. The vector "bar code" is an oligonucleotide sequence within the vector which is unique to each individual clone of a library. The bar code enables sorting of the library in phys. space by hybridization to nucleic acid **arrays** which are complementary to library bar code sequences. The bar code unique to each clone together with the unique position of each complementary bar code in a nucleic acid **array** provides a method for direct retrieval of a gene having a function of interest in any given readout assay. Further, each unique bar code can serve as a specific primer for PCR and/or sequencing of a desired clone in a library. It is the ability to detect a biol. readout in a readout cell line which enables the user to identify genes having specific functions. It is able to directly screen mammalian cDNA libraries with an av. size of 106 clones through automation. Digestion of vectors is involved with restriction endonucleases. The methods set forth herein are suitable for application in a high throughput format for identification of genes and their functions simultaneously. Discovery of new genes and their functions permits development of diagnostics for early detection of diseases. This method permits discovery of discovery of disease-assocd. genes and is suitable for use with antisense libraries.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Affymetrix Inc	1997			EP 0799897 A1	HCAPLUS
Brenner	1997			US 5604097 A	HCAPLUS
Clark	1987			US 4675285 A	HCAPLUS
Fodor	1995			US 5445934 A	HCAPLUS
King	1997			US 5654150 A	HCAPLUS
Rhode Island Hospital	1993			EP 0534619 A2	HCAPLUS
Shoemaker	1996	14	450	Nature Genetics	HCAPLUS

L138 ANSWER 29 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:691243 HCAPLUS
DN 131:307694
TI Biallelic markers for use in constructing a **high density** disequilibrium map of the human **genome**
IN Cohen, Daniel; Blumenfeld, Marta; Chumakov, Ilya
PA Genset, Fr.
SO PCT Int. Appl., 229 pp.

CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9954500	A2	19991028	WO 1999-IB822	19990421
	WO 9954500	A3	20000316		

W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

	AU 9934386	A1	19991108	AU 1999-34386	19990421

PRAI US 1998-82614 19980421
US 1998-109732 19981123
WO 1999-IB822 19990421

AB The present invention relates to **genomic** maps comprising biallelic markers, new biallelic markers, and methods of using biallelic markers. Primers hybridizing to regions flanking these biallelic markers are also provided. This invention provides polynucleotides and methods suitable for genotyping a nucleic acid contg. sample for one or more biallelic markers of the invention. Further, the invention provides a no. of methods utilizing the biallelic markers of the invention including methods to detect a statistical correlation between a biallelic marker allele and a phenotype and/or between a biallelic marker haplotype and a phenotype. The compns. and methods of the invention also find use in the identification of targets for the development of pharmaceutical agents and diagnostic methods, as well as the characterization of differential efficacious responses to and side effects from pharmaceutical agents acting on a disease (e.g., Alzheimer's disease, prostate cancer, or asthma) as well as other treatments. The invention claims 3934 biallelic marker sequences, as well as the primer pairs for amplification and detection of each marker; however, the Sequence Listing is not actually provided in the document.

L138 ANSWER 30 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:616046 HCAPLUS
DN 131:332905
TI Cluster analysis and display of **genome**-wide expression patterns. [Erratum to document cited in CA130:163878]
AU Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CS Dep. Genetics, Howard Hughes Medical Institute, Stanford Univ. School Medicine, Stanford, CA, 94305, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1999), 96(19), 10943
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Two refs. were omitted. Ref. 1 [Weinstein, J. N., Myers, T. G., O'Connor, P. M., Friend, S. H., Fornace, A. J., Jr., Kohn, K. W., Fojo, T., Bates, S. E., Rubinstein, L. V., Anderson, N. L., et al. (1997) science 275, 343-349] refers to a precedent for coloring of data tables following cluster anal. Ref. 2 [Wen, X., Fuhrman, S., Michaels, G. S., Carr, D. B., Smith, S., Barker, J. L Somogyi, R. (1998) Proc. Natl. Acad. Sci. USA 95, 334-339] refers to an earlier example of applying cluster anal. to gene expression data.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Weinstein, J	1997	275	343	Science	HCAPLUS

Wen, X |1998 |95 | |Proc Natl Acad Sci U|HCAPLUS

L138 ANSWER 31 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:566264 HCAPLUS
DN 131:167361
TI Cellular **arrays** for rapid molecular profiling
IN Kallioniemi, Olli; Kononen, Juha; Leighton, Stephen B.; Sauter, Guido
PA The United States of America as Represented by the Secretary Department of Health, USA
SO PCT Int. Appl., 74 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 3

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9944062	A1	19990902	WO 1999-US4000	19990224
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 9929735	A1	19990915	AU 1999-29735	19990224
EP 1066517	A1	20010110	EP 1999-910986	19990224
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRAI US 1998-75979 19980225
US 1998-106038 19981028
WO 1999-US4000 19990224

AB A method is disclosed for rapid mol. profiling of tissue or other cellular specimens by placing a donor specimen in an assigned location in a recipient **array**, providing copies of the **array**, and performing a different biol. anal. of each copy. In one embodiment, the copies of the **array** are formed by placing elongated specimens in a three dimensional matrix, and cutting sections from the matrix to form multiple copies of a two dimensional **array** that can then be subjected to the different biol. analyses. Alternatively, the **array** can be formed from cell suspensions such that identical multiple copies of an **array** are formed, in which corresponding positions in the copies of the **array** have samples from the same or similar specimen. The results of the different biol. analyses are compared to det. if there are correlations between the results of the different biol. analyses at each assigned location. In some embodiments, the specimens may be tissue specimens from different tumors, which are subjected to multiple parallel mol. (including genetic and immunol.) analyses. The results of the parallel analyses are then used to detect common mol. characteristics of the tumor type, which can subsequently be used in the diagnosis or treatment of the disease. The biol. characteristics of the tissue can be correlated with clin. or other information, to detect characteristics assocd. with the tissue, such as susceptibility or resistance to particular types of drug treatment. Other examples of suitable tissues which can be placed in the matrix include tissue from transgenic or model organisms, or cellular suspensions (such as cytol. prepns. or specimens of liq. malignancies or cell lines).

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Battifora	1989			US 4820504 A	
Battifora	1991			US 5002377 A	
Furmanski	1990			US 4914022 A	
Southern	1997			US 5700637 A	HCAPLUS

L138 ANSWER 32 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:495415 HCAPLUS
DN 131:140461
TI A method combining features of random amplified polymorphic DNA and **arrayed** primer extension for nucleic acid analysis
IN Ulfendahl, Per Johan
PA Amersham Pharmacia Biotech AB, Swed.
SO PCT Int. Appl., 39 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 9939001	A2	19990805	WO 1999-EP918	19990202
WO 9939001	A3	19991007		

W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AU 9930276	A1	19990816	AU 1999-30276	19990202
EP 1051523	A2	20001115	EP 1999-911663	19990202

R: BE, CH, DE, DK, FR, GB, IT, LI, NL, SE

PRAI EP 1998-300741 19980202
WO 1999-EP918 19990202
AB A nucleic acid anal. method comprises: using a primer to amplify the nucleic acid; providing an **array** of probes, each probe comprising a sequence identical to the primer and an adjacent sequence; applying fragments of the amplifier nucleic acid under hybridization conditions to the **array**; effecting enzymic chain extension of any probe where the adjacent sequence matches that of a hybridized fragment of the amplified nucleic acid; and observing the location of probes of the **array** while chain extension has taken place. The invention method performed in microtiter plates (MTP) with both fluorescein labeled dCTP and anti-fluorescein antibodies and detected by using para-nitrophenyl phosphate (pNpp). The method is useful for characterization, classification, identification, and typing of different DNA-contg. organisms. The method was demonstrated by the identification of Escherichia coli strains BL21 and C1a with their **genomic** DNA patterns.

L138 ANSWER 33 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:470434 HCAPLUS
DN 131:224009
TI DNA chips: promising toys have become powerful tools
AU Gerhold, David; Rushmore, Thomas; Caskey, C. Thomas
CS Human Genetics Dept., Merck and Co., West Point, PA, 19486, USA
SO Trends Biochem. Sci. (1999), 24(5), 168-173
CODEN: TBSCDB; ISSN: 0376-5067
PB Elsevier Science Ltd.
DT Journal; General Review
LA English
AB A review with 28 refs. DNA chips are glass surfaces that represent thousands of DNA fragments **arrayed** at discrete sites. Hybridization of RNA or DNA-derived samples to DNA chips allows us to monitor expression of mRNAs or the occurrence of polymorphisms in **genomic** DNA. The technol. holds great promise for identifying gene polymorphisms that predispose man to disease, gene regulation events involved in disease progression, and more-effective disease treatments.
RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Aspinall, J	1995	154	622	J Urol	MEDLINE
Blanchard, A	1996	11	687	Biosens Bioelectron	HCAPLUS
Chee, M	1996	274	610	Science	HCAPLUS
Cho, R	1998	2	65	Mol Cell	HCAPLUS
Cronin, M	1996	7	244	Hum Mutat	HCAPLUS
Drmanac, S	1998	16	54	Nat Biotechnol	MEDLINE
Edman, C	1997	25	4907	Nucleic Acids Res	HCAPLUS
Eisen, M	1998	95	14863	Proc Natl Acad Sci U	HCAPLUS
Gao, C	1997	19	307	BioEssays	HCAPLUS
Hacia, J	1996	14	441	Nat Genet	HCAPLUS
Joos, B	1997	247	96	Anal Chem	HCAPLUS
Karp, P	1998	23	114	Trends Biochem Sci	HCAPLUS
Kozal, M	1996	2	753	Nat Med	HCAPLUS
Lennon, G	1991	7	314	Trends Genet	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Marshall, A	1998	16	27	Nat Biotechnol	HCAPLUS
Mashimo, T	1998	95	11307	Proc Natl Acad Sci U	HCAPLUS
McConkey, E	1993			Human Genetics The M	
Ortiz de Montellano, P	1995		474	Cytochrome P450s Str	
Pease, A	1994	91	5022	Proc Natl Acad Sci U	HCAPLUS
Ramsay, G	1998	16	40	Nat Biotechnol	HCAPLUS
Schena, M	1995	270	467	Science	HCAPLUS
Shumaker, J	1996	7	346	Hum Mutat	HCAPLUS
Southern, E	1975	98	503	J Mol Biol	HCAPLUS
Timofeev, E	1996	24	3142	Nucleic Acids Res	HCAPLUS
Wang, D	1998	280	1077	Science	HCAPLUS
Wang, F	1996	56	3634	Cancer Res	HCAPLUS
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS

L138 ANSWER 34 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:468653 HCAPLUS
DN 131:98477
TI Enhanced discrimination of perfect matches from mismatches using a modified DNA ligase
IN Baidya, Narayan
PA Hyseq, Inc., USA
SO PCT Int. Appl., 112 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9936567	A2	19990722	WO 1999-US176	19990114
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9925577	A1	19990802	AU 1999-25577	19990114
PRAI	US 1998-7300	19980114			
	WO 1999-US176	19990114			

AB The invention relates to methods using a modified DNA ligase which increases the discrimination of perfect matches from mismatches for complementary polynucleotides. The modified ligase enhances discrimination in a no. of ways, for example, the ligase may increase the difference in the on rates and/or the off rates between a perfect match product and a mismatch product (a kinetic effect); or the ligase may increase the binding energy difference between a perfect match and a mismatch (a free energy [.DELTA.G] effect); or the ligase may itself

discriminate between perfect matches and mismatches (.DELTA.G or kinetic effect); or some combination of these and other factors. In the present invention, sequencing by hybridization (SBH) is applied to the efficient identification and sequencing of one or more nucleic acid samples. The invention provides a method for detecting a target nucleic acid species including the steps of providing an **array** of probes affixed to a substrate and a plurality of labeled probes wherein each labeled probe is selected to have a first nucleic acid sequence which is complementary to a first portion of a target nucleic acid and wherein the nucleic acid sequence of at least one probe affixed to the substrate is complementary to a second portion of the nucleic acid sequence of the target, the second portion being adjacent to the first portion; applying a target nucleic acid to the **array** under suitable conditions for hybridization of probe sequences to complementary sequences; introducing a labeled probe to the **array**; hybridizing a probe affixed to the substrate to the target nucleic acid; hybridizing the labeled probe to the target nucleic acid; affixing the labeled probe to an adjacently hybridized probe in the **array**; and detecting the labeled probe affixed to the probe in the **array**. The procedure has many applications in nucleic acid diagnostics, forensics, and gene mapping. It may also be used to identify mutations responsible for genetic disorders and other traits, to assess biodiversity, and to produce many other types of data dependent on nucleic acid sequence.

L138 ANSWER 35 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:416549 HCAPLUS
DN 131:180301
TI Promoter analysis of co-regulated genes in the yeast **genome**
AU Zhang, Michael Q.
CS Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 11724, USA
SO Comput. Chem. (Oxford) (1999), 23(3-4), 233-250
CODEN: COCHDK; ISSN: 0097-8485
PB Elsevier Science Ltd.
DT Journal
LA English
AB The use of **high d.** DNA **arrays** to monitor gene expression at a **genome**-wide scale constitutes a fundamental advance in biol. In particular, the expression pattern of all genes in Saccharomyces cerevisiae can be interrogated using **microarray** anal. where cDNAs are hybridized to an **array** of more than 6000 genes in the yeast **genome**. In an effort to build a comprehensive Yeast Promoter Database and to develop new computational methods for mapping upstream regulatory elements, we started recently in an on going collaboration with exptl. biologists on anal. of large-scale expression data. It is well known that complex gene expression patterns result from dynamic interacting networks of genes in the genetic regulatory circuitry. Hierarchical and modular organization of regulatory DNA sequence elements are important information for our understanding of combinatorial control of gene expression. As a **bioinformatics** attempt in this new direction, we have done some computational exploration of various initial exptl. data. We will use cell-cycle regulated gene expression as a specific example to demonstrate how one may ext. promoter information computationally from such **genome**-wide screening. Full report of the expts. and of the complete anal. will be published elsewhere when all the expts. are to be finished later in this year (Spellman, P.T., et al. 1998. Mol. Biol. Cell 9, 3273-3297).

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Aerne, B	1998	9	945	Mol Biol Cell	HCAPLUS
Althoefer, H	1995	15	5917	Mol Cell Biol	HCAPLUS
Amon, A	1993	74	993	Cell	HCAPLUS
Andrews, B	1992	70	1073	Biochem Cell Biol	HCAPLUS
Andrews, B	1989	342	830	Nature	HCAPLUS
Andrews, B	1993	261	1543	Science	MEDLINE

Bender, A	1987	50	681	Cell	HCAPLUS
Bohm, S	1997	25	2464	Nucl Acid Res	HCAPLUS
Breeden, L	1987	48	389	Cell	HCAPLUS
Breeden, L	1988	4	249	Trends Genet	HCAPLUS
Cho, R	1998	2	65	Mol Cell	HCAPLUS
DeRisi, J	1997	278	680	Science	HCAPLUS
Dohrmann, P	1992	6	93	Genes & Dev	HCAPLUS
Dohrmann, P	1996	16	1746	Mol Cell Biol	HCAPLUS
Epstein, C	1992	6	1695	Genes & Dev	HCAPLUS
Fondrat, C	1996	12	363	CABIOS	HCAPLUS
Heinemeyer, T	1998	26	364	Nucl Acid Res	
Hereford, L	1982	30	305	Cell	HCAPLUS
Hertz, G	1990	6	81	CABIOS	HCAPLUS
Iyer, V	1995	14	2570	EMBO J	HCAPLUS
Koch, C	1994	6	451	Curr Op Cell Biol	HCAPLUS
Koch, C	1993	261	1551	Science	HCAPLUS
Kovacech, B	1996	16	3264	Mol Cell Biol	HCAPLUS
Kuo, M	1994	14	348	Mol Cell Biol	HCAPLUS
Lawrence, C	1993	262	208	Science	HCAPLUS
Lowndes, N	1991	350	247	Nature	HCAPLUS
Lydall, D	1991	5	2405	Genes & Dev	HCAPLUS
McBride, H	1997	17	2669	Mol Cell Biol	HCAPLUS
McInerny, C	1997	11	1277	Genes & Dev	HCAPLUS
McIntosh, E	1993	24	185	Curr Genet	MEDLINE
McIntosh, E	1991	11	329	Mol Cell Biol	HCAPLUS
Moll, T	1991	66	743	Cell	HCAPLUS
Nait-Kaoudjt, R	1997	244	301	Eur J Biochem	HCAPLUS
Nasmyth, K	1985	42	225	Cell	HCAPLUS
Nasmyth, K	1987	49	549	Cell	HCAPLUS
Nasmyth, K	1991	66	995	Cell	HCAPLUS
Nasmyth, K	1993	5	166	Curr Opin Cell Biol	HCAPLUS
Neuwald, A	1995	4	1618	Protein Sci	HCAPLUS
Ogas, J	1991	66	1015	Cell	HCAPLUS
Osley, M	1991	60	827	Annu Rev Biochem	HCAPLUS
Osley, M	1986	45	537	Cell	HCAPLUS
Passmore, S	1989	3	921	Genes & Dev	HCAPLUS
Price, C	1991	218	543	J Mol Biol	HCAPLUS
Reed, S	1992	8	529	Annu Rev Cell Biol	HCAPLUS
Roth, F				Preprint	
Schwob, E	1993	7	1160	Genes & Dev	HCAPLUS
Sidorova, J	1993	13	1069	Mol Cell Biol	HCAPLUS
Spellman, P	1998	9	3273	Mol Biol Cell	HCAPLUS
Stein, L	1998		791	Current protocols in	
Stormo, G	1990	183	211	Methods Enzymol	HCAPLUS
Taylor, I	1997	272	1	J Mol Biol	HCAPLUS
Tebb, G	1993	7	517	Genes & Dev	HCAPLUS
Treisman, R	1992	2	221	Curr Opin Genet Dev	HCAPLUS
Van Helden, J	1998	281	827	J Mol Biol	HCAPLUS
White, J	1987	171	223	Exp Cell Res	HCAPLUS
Wynne, J	1992	20	3297	Nucl Acid Res	HCAPLUS
Xu, R	1997	5	349	Protein Structure	HCAPLUS
Zhang, M	1998	8	319	Genome Research	HCAPLUS
Zhang, M				Large scale gene exp	
Zhu, J	1998			First International	

L138 ANSWER 36 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:359642 HCAPLUS
DN 131:14828
TI Method of parallel screening for insertion mutants and a kit to perform this method
IN Maes, Tamara; Gerats, Tom
PA Vlaams Interuniversitair Instituut Voor Biotechnologie VZM, Belg.
SO PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9927085	A2	19990603	WO 1998-EP7551	19981123
	WO 9927085	A3	19990812		
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	AU 9920496	A1	19990615	AU 1999-20496	19981123
	EP 1034261	A2	20000913	EP 1998-965172	19981123
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
PRAI	EP 1997-203680	19971125			
	WO 1998-EP7551	19981123			

AB The current invention is a novel approach termed "parallel screening," allowing simultaneous screening a population for insertions in all genes cloned from that or a closely related organism, by hybridizing target sequences with all the insertion element flanking sequences amplified from the population. In order to test this approach the flowering plant Petunia hybrida was used as a model system. Petunia hybrida line W137 contains a high copy no. of the endogenous transposable element dTph1 and has been presented as a genetic tool before. A 3D library of the plant **genomic** DNA of 1000 Petunia hybrida W137 plants was generated as described by Koes et al. (1995). The 3D library consists of 30 pools of DNA from a 100 plants each. These were used to generate 30 pools of insertion flanking sequences by nested iPCR using a set of transposon specific primers or by Transposon Display PCR. Insertions into a gene were detected by hybridizing the amplified insertion flanking sequences fixed to a filter with a gene specific probe, an approach termed simple screening for insertion elements. Alternatively, the amplified insertion element flanking sequences were labeled and used as a probe to hybridize a filter displaying multiple gene targets, an approach termed parallel screening for insertion elements, which allows the simultaneous screening for insertions in all genes of an organism, appearing in a population of insertion mutants.

L138 ANSWER 37 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:232102 HCAPLUS
DN 130:262708
TI Biosensors in biomedical research. Development and applications of **gene chips**
AU Certa, Ulrich; Hochstrasser, Remo; Langen, Hanno; Buess, Martin; Moroni, Christoph
CS Department PRPG, F. Hoffmann-La-Roche Ltd., Basel, CH-4070, Switz.
SO Chimia (1999), 53(3), 57-61
CODEN: CHIMAD; ISSN: 0009-4293
PB Neue Schweizerische Chemische Gesellschaft
DT Journal; General Review
LA English
AB A review with 6 refs. is given. Nucleic-acid hybridization techniques are a central tool for the genetic anal. of biol. systems. **Gene chips** are complex **arrays** of recombinant plasmids or oligonucleotides immobilized on a glass chip of only 1 cm2. This technol. allows, for the first time, the multiparallel expression-anal. of thousands of genes. **Gene chips** will be indispensable tools for the upcoming anal. of the human **genome**, once the entire sequence is known.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File

Buess, M	1999			to be published in O	
de Saizieu, A	1998	16	45	Nature Biotechnology	HCAPLUS
Fodor, S	1993	364	555	Nature (London)	MEDLINE
Shena, M	1995	270	467	Science	
Wang, S	1996	271	20580	J Biol Chem	HCAPLUS
Wodicka, L	1997	15	1359	Nature Biotechnology	HCAPLUS

L138 ANSWER 38 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:53122 HCAPLUS
DN 130:247490
TI High density synthetic oligonucleotide **arrays**
AU Lipshutz, Robert J.; Fodor, Stephen P. A.; **Gingeras, Thomas R.**; Lockhart, David J.
CS Affymetrix, Inc., Santa Clara, CA, 95051, USA
SO Nat. Genet. (1999), 21(1, Suppl.), 20-24
CODEN: NGENEC; ISSN: 1061-4036
PB Nature America
DT Journal; General Review
LA English
AB A review, with 32 refs. Exptl. genomics involves taking advantage of sequence information to investigate and understand the workings of genes, cells and organisms. We have developed an approach in which sequence information is used directly to design high-d., two-dimensional arrays of synthetic oligonucleotides. The GeneChip probe arrays are made using spatially patterned, light-directed combinatorial chem. synthesis, and contain up to hundreds of thousands of different oligonucleotides on a small glass surface. The arrays have been designed and used for quant. and highly parallel measurements of gene expression, to discover polymorphic loci and to detect the presence of thousands of alternative alleles. Here, we describe the fabrication of the arrays, their design and some specific applications to high-throughput genetic and cellular anal.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Beecher, J	1997	76	597	Polymeric Materials	HCAPLUS
Bowtell, D	1999	21	25	Nature Genet	HCAPLUS
Chakravarti, A	1999	21	56	Nature Genet	HCAPLUS
Chee, M	1996	274	610	Science	HCAPLUS
Cheung, V	1999	21	15	Nature Genet	HCAPLUS
Cho, R	1998	2	65	Mol Cell	HCAPLUS
Cho, R	1998	95	3752	Proc Natl Acad Sci U	HCAPLUS
de Saizleu, A	1998	16	45	Nature Biotechnol	
Duggan, D	1999	21	10	Nature Genet	HCAPLUS
Fodor, S	1993	364	555	Nature	MEDLINE
Fodor, S	1991	251	767	Science	HCAPLUS
Fodor, S	1997	277	393	Science	HCAPLUS
Gingeras, T	1998	8	435	Genome Res	HCAPLUS
Gray, N	1998	281	533	Science	HCAPLUS
Gunderson, K				Genome Res (in press	
Gunthard, H	1998	14	869	AIDS Res Hum Retrovi	HCAPLUS
Hacia, J	1999	21	42	Nature Genet	HCAPLUS
Kozal, M	1996	7	753	Nature Med	
Lockhart, D	1996	14	1675	Nature Biotechnol	HCAPLUS
Mack, D	1998		85	Biology of Tumors	HCAPLUS
McGall, G	1997	119	5081	J Am Chem Soc	HCAPLUS
McGall, G	1996	93	13555	Proc Natl Acad Sci U	HCAPLUS
Pease, A	1994	91	5022	Proc Natl Acad Sci U	HCAPLUS
Pirrung, M	1998	63	241	J Organic Chem	HCAPLUS
Sapolsky, R	1996	33	445	Genomics	HCAPLUS
Shoemaker, D	1996	14	450	Nature Genet	HCAPLUS
Southern, E	1992	13	1008	Genomics	HCAPLUS
Troesch, A				J Clin Microbiol (in	
Wang, D	1998	280	1077	Science	HCAPLUS
Winzeler, E	1998	281	1194	Science	HCAPLUS

Wodicka, L	1997	15	1359	Nature Biotechnol	HCAPLUS
Zhu, H				Proc Natl Acad Sci U	

L138 ANSWER 39 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1999:46849 HCAPLUS
DN 130:262729
TI Mycobacterium species identification and rifampin resistance testing with high-density DNA probe **arrays**
AU Troesch, A.; Nguyen, H.; Miyada, C. G.; Desvarenne, S.; **Gingeras, T. R.**; Kaplan, P. M.; Cros, P.; Mabilat, C.
CS bioMerieux, Marcy-L'Etoile, 69280, Fr.
SO J. Clin. Microbiol. (1999), 37(1), 49-55
CODEN: JCMIDW; ISSN: 0095-1137
PB American Society for Microbiology
DT Journal
LA English
AB Species identification within the genus Mycobacterium and subsequent antibiotic susceptibility testing still rely on time-consuming, culture-based methods. Despite the recent development of DNA probes, which greatly reduce assay time, there is a need for a single platform assay capable of answering the multitude of diagnostic questions assocd. with this genus. We describe the use of a DNA probe array based on two sequence databases: one for the species identification of mycobacteria (82 unique 16S rRNA sequences corresponding to 54 phenotypical species) and the other for detecting Mycobacterium tuberculosis rifampin resistance (rpoB alleles). Species identification or rifampin resistance was detd. by hybridizing fluorescently labeled, amplified genetic material generated from bacterial colonies to the array. Seventy mycobacterial isolates from 27 different species and 15 rifampin-resistant M. tuberculosis strains were tested. A total of 26 of 27 species were correctly identified as well as all of the rpoB mutants. This parallel testing format opens new perspectives in terms of patient management for bacterial diseases by allowing a no. of genetic tests to be simultaneously run.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Banerjee, A	1994	263	227	Science	HCAPLUS
Boddinghaus, B	1990	28	1751	J Clin Microbiol	MEDLINE
Chee, M	1996	274	610	Science	HCAPLUS
Cole, S	1994	2	411	Trends Microbiol	MEDLINE
Cooksey, R	1997	35	1281	J Clin Microbiol	HCAPLUS
Cronin, M	1996	7	244	Hum Mutat	HCAPLUS
Fodor, S	1993	364	555	Nature	MEDLINE
Gingeras, T	1998	8	435	Genome Res	HCAPLUS
Heym, B	1995	15	235	Mol Microbiol	HCAPLUS
Horsburgh, C	1991	324	1332	N Engl J Med	
Jenkins, P	1991	70	137S	J Appl Bacteriol Sym	
Kapur, V	1994	32	1095	J Clin Microbiol	HCAPLUS
Kent, P	1985			Public health mycoba	
Kirschner, P	1993	31	2882	J Clin Microbiol	HCAPLUS
Kirschner, P	1996	34	304	J Clin Microbiol	HCAPLUS
Koukila-Kahkola, P	1995	45	549	Int J Syst Bacteriol	MEDLINE
Kozal, M	1996	2	753	Nat Med	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Mdluli, K	1998	280	1607	Science	HCAPLUS
Raviglione, M	1995	273	220	JAMA	MEDLINE
Roberts, G	1991	5th e	304	Manual of clinical m	
Scorpio, A	1996	2	662	Nat Med	HCAPLUS
Springer, B	1996	34	296	J Clin Microbiol	HCAPLUS
Sreevatsan, S	1997	41	1677	Antimicrob Agents Ch	HCAPLUS
Sreevatsan, S	1997	41	636	Antimicrob Agents Ch	HCAPLUS
Telenti, A	1993	341	647	Lancet	HCAPLUS
Tortoli, E	1997	35	697	J Clin Microbiol	HCAPLUS
Whelen, A	1995	33	556	J Clin Microbiol	HCAPLUS
Wilson, T	1996	19	1025	Mol Microbiol	HCAPLUS

Yates, M	1997	1	75	Int J Tuberc Lung Di	MEDLINE
Zhang, Y	1992	358	501	Nature	

L138 ANSWER 40 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:805587 HCAPLUS
DN 130:163878
TI Cluster analysis and display of **genome**-wide expression patterns
AU Eisen, Michael B.; Spellman, Paul T.; Brown, Patrick O.; Botstein, David
CS Department of Genetics, Howard Hughes Medical Institute, Stanford University School of Medicine, Stanford, CA, 94305, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1998), 95(25), 14863-14868
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB A system of cluster anal. for **genome**-wide expression data from DNA **microarray** hybridization is described that uses std. statistical algorithms to arrange genes according to similarity in pattern of gene expression. The output is displayed graphically, conveying the clustering and the underlying expression data simultaneously in a form intuitive for biologists. We have found in the budding yeast Saccharomyces cerevisiae that clustering gene expression data groups together efficiently genes of known similar function, and we find a similar tendency in human data. Thus patterns seen in **genome** -wide expression expts. can be interpreted as indications of the status of cellular processes. Also, coexpression of genes of known function with poorly characterized or novel genes may provide a simple means of gaining leads to the functions of many genes for which information is not available currently.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Cherry, J	1997	387	67	Nature (London)	HCAPLUS
Chu, S	1998	282	699	Science	HCAPLUS
Derisi, J	1997	278	680	Science	HCAPLUS
Hereford, L	1981	24	367	Cell	HCAPLUS
Iyer, V	1998			Science in press	
Kief, D	1981	1	1007	Mol Cell Biol	HCAPLUS
Kohonen, T	1997			Self-Organizing Maps	
Kraakman, L	1993	239	196	Mol Gen Genet	HCAPLUS
Kwast, K	1998	201	1177	J Exp Biol	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Schena, M	1996	93	10614	Proc Natl Acad Sci U	HCAPLUS
Schena, M	1995	270	467	Science	HCAPLUS
Shalon, D	1996	6	639	Genome Res	HCAPLUS
Sokal, R	1958	38	1409	Univ Kans Sci Bull	
Spellman, P	1998			Mol Biol Cell in pre	
Velculescu, V	1995	270	484	Science	HCAPLUS

L138 ANSWER 41 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:798284 HCAPLUS
DN 130:192430
TI Deciphering molecular circuitry using high-density DNA **arrays**
AU Mack, David H.; Tom, Edward Y.; Mahadev, Mamatha; Dong, Helin; Mittmann, Michael; Dee, Suzanne; Levine, Arnold J.; **Gingeras, Thomas R.**; Lockhart, David J.
CS Program in Cancer Biology, Santa Clara, CA, 95051, USA
SO Pezcoller Found. Symp. (1998), 9(Biology of Tumors), 85-108
CODEN: PFSYES; ISSN: 0961-785X
PB Plenum Publishing Corp.
DT Journal
LA English
AB DNA arrays contg. oligonucleotides complementary to > 6,500 human EST's were used to generate normal and breast cancer specific gene expression profiles. More than 1,500 expressed genes were detected in both cell

types. Over 300 genes demonstrated significantly different levels of expression between normal and transformed cells. Increased mRNA levels were obsd. for the Her2/neu oncogene and genes involved in tis signal transduction, including Grb-7, Ras, Raf, Mek, and ERK. In addn., a simple categorization of the expression changes revealed patterns characteristic of loss of wild-type p53 function. Genotyping of the p53 locus using a DNA resequencing array reveled inactivating mutation in the p53 DNA-binding domain and loss of heterogeneity. These data demonstrate a general array-hybridization approach to deciphering biochem. pathways and generating testable hypotheses concerning the mechanisms of cell growth and differentiation.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Adams, M	1995	377	3	Nature	HCAPLUS
Alblas, J	1993	30	22235	Journal of Biologica	
Boguski, M	1993	4	332	Nature Genetics	HCAPLUS
Chee, M	1996	5287	610	Science	
Clark, G	1995	1	133	Breast Cancer Resear	
Coussens, L	1985	4730	1132	Science	
Earp, H	1995	1	115	Breast Cancer Resear	
Fodor, S	1991	251	767	Science	HCAPLUS
Hackett, A	1977	6	1795	Journal of the Natio	
King, C	1985	4717	974	Science	
Koleske, A	1995	5	1381	Proceedings of the N	
Kraus, M	1989	23	9193	Proceedings of the N	
Lasfargues, E	1978	4	967	Journal of the Natio	
Lemoine, N	1992	6	1116	British Journal of C	
Levine, A	1997	3	323	Cell	
Li, N	1993	6424	85	Nature	
Li, S	1995	26	15693	Journal of Biologica	
Lisanti, M	1995	1	121	Molecular Membrane B	
Lockhart, D	1996	13	1675	Nature Biotechnology	
Marshall, M	1995	13	1311	Faseb Journal	
Schena, M	1995	270	467	Science	HCAPLUS
Sivaraman, V	1997	99	1478	J Clin Invest	HCAPLUS
Slamon, D	1987	4785	177	Science	
Slamon, D	1989	4905	707	Science	
Stein, D	1994	13	1331	EMBO J	HCAPLUS
Styles, J	1990	2	320	International Journa	
Van Biesen, T	1995	6543	781	Nature	
Velculescu, V	1996	6 Pt	858	Clinical Chemistry	
Velculescu, V	1995	270	484	Science	HCAPLUS
Wallasch, C	1995	14	4267	EMBO J	HCAPLUS
Winitz, S	1993	26	19196	Journal of Biologica	
Zhang, L	1997	276	1268	Science	HCAPLUS

L138 ANSWER 42 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:765634 HCAPLUS
DN 130:137555
TI Cellular gene expression altered by human cytomegalovirus: global monitoring with oligonucleotide **arrays**
AU Zhu, Hua; Cong, Jian-Ping; Mamtora, Gargi; **Gingeras, Thomas**; Shenk, Thomas
CS Howard Hughes Medical Institute, Department of Molecular Biology, Princeton University, Princeton, NJ, 08544, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1998), 95(24), 14470-14475
CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Mechanistic insights to viral replication and pathogenesis generally have come from the anal. of viral gene products, either by studying their biochem. activities and interactions individually or by creating mutant viruses and analyzing their phenotype. Now it is possible to identify and

catalog the host cell genes whose mRNA levels change in response to a pathogen. We have used DNA **array** technol. to monitor the level of .apprxeq.6,600 human mRNAs in uninfected as compared with human cytomegalovirus-infected cells. The level of 258 mRNAs changed by a factor of 4 or more before the onset of viral DNA replication. Several of these mRNAs encode gene products that might play key roles in virus-induced pathogenesis, identifying them as intriguing targets for further study.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Adams, J	1997	29	861	Int J Biochem Cell B	HCAPLUS
Ahn, K	1997	6	613	Immunity	HCAPLUS
Ahn, K	1996	93	10990	Proc Natl Acad Sci U	HCAPLUS
Baldick, C	1996	70	6097	J Virol	HCAPLUS
Borrego, F	1998	187	813	J Exp Med	HCAPLUS
Bouffard, P	1996	23	1838	J Rheumatol	MEDLINE
Braud, V	1997	27	1164	Eur J Immunol	HCAPLUS
Braud, V	1998	391	795	Nature (London)	HCAPLUS
Bresnahan, W	1996	224	150	Virology	HCAPLUS
Britt, W	1996		2493	Fields Virology	
Chapman, A	1994	81	435	Immunology	HCAPLUS
Chee, M	1990	344	774	Nature (London)	HCAPLUS
Chee, M	1996	274	610	Science	HCAPLUS
Croxtall, J	1996	220	491	Biochem Biophys Res	HCAPLUS
Croxtall, J	1996	52	351	Biochem Pharmacol	HCAPLUS
Crump, J	1992	6	674	Am J Respir Cell Mol	HCAPLUS
Dittmer, D	1997	71	1629	J Virol	HCAPLUS
Finkelstein, Y	1997	148	205	Ann Med Interne (Par	MEDLINE
Fodor, S	1991	251	767	Science	HCAPLUS
Fodor, S	1993	364	555	Science	MEDLINE
Hengel, H	1997	6	623	Immunity	HCAPLUS
Herrath, M	1996	8	878	Curr Opin Immunol	
Igarashi, T	1995	22	33	Autoimmunity	HCAPLUS
Iwamoto, G	1990	85	1853	J Clin Invest	HCAPLUS
Jault, F	1995	69	6697	J Virol	HCAPLUS
Jones, T	1997	71	2970	J Virol	HCAPLUS
Jones, T	1996	93	11327	Proc Natl Acad Sci U	HCAPLUS
Kapasi, K	1998	62	3603	J Virol	
Kondo, K	1996	93	11137	Proc Natl Acad Sci U	HCAPLUS
Lawler, J	1998	101	982	J Clin Invest	HCAPLUS
Lawson, C	1991	72	426	Immunology	HCAPLUS
Lipshutz, R	1995	19	442	BioTechniques	HCAPLUS
Liu, B	1992	66	4434	J Virol	HCAPLUS
Lockhart, D	1996	14	1675	Nat Biotechnol	HCAPLUS
Lu, M	1996	70	8850	J Virol	HCAPLUS
Malone, C	1990	64	1498	J Virol	HCAPLUS
McCarthy, R	1980	90	558	Am J Ophthalmol	MEDLINE
Mocarski, E	1996		2447	Fields Virology	
O'Donoghue, H	1990	71	20	Immunology	HCAPLUS
Pease, A	1994	91	5022	Proc Natl Acad Sci U	HCAPLUS
Pizzorno, M	1988	62	1167	J Virol	HCAPLUS
Price, P	1993	78	14	Immunology	MEDLINE
Quinnan, G	1984	101	478	Ann Intern Med	
Rayburn, H	1997	386	514	Nature (London)	
Rogers, B	1985	55	527	J Virol	
Shibutani, T	1997	100	2054	J Clin Invest	HCAPLUS
Sinclair, J	1996	39	293	Intervirology	MEDLINE
Soderberg-Naucler, C	1997	91	119	Cell	HCAPLUS
Steingrimsson, E	1994	8	256	Nat Genet	HCAPLUS
Stenberg, R	1990	64	1556	J Virol	HCAPLUS
Tassabehji, M	1994	8	251	Nat Genet	HCAPLUS
Tsutsui, Y	1993	143	804	Am J Pathol	MEDLINE
Tuszynski, G	1995	18	71	BioEssays	
Welch, A	1991	65	3915	J Virol	HCAPLUS

Wiertz, E	1996	84	769	Cell	HCAPLUS
Wodicka, L	1997	15	1359	Nat Biotechnol	HCAPLUS
Yurochko, A	1997	71	5051	J Virol	HCAPLUS
Zhu, H	1997	94	13985	Proc Natl Acad Sci U	HCAPLUS

L138 ANSWER 43 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:667795 HCAPLUS
DN 130:78127
TI Overview of DNA chip technology
AU Lemieux, Bertrand; Aharoni, Asaph; Schena, Mark
CS Department of Plant and Soil Sciences, University of Delaware, Newark, DE, 19717, USA
SO Mol. Breed. (1998), 4(4), 277-289
CODEN: MOBRFL; ISSN: 1380-3743
PB Kluwer Academic Publishers
DT Journal; General Review
LA English
AB A review, with 50 refs., is given on DNA **microarrays** produced on glass surfaces at densities of 400-250,000 features/cm2. DNA chip technol. uses microscopic **arrays** (**microarrays**) of mols. immobilized on solid surfaces for biochem. anal. **Microarrays** can be used for expression anal., polymorphism detection, DNA resequencing, and genotyping on a **genomic** scale. Advanced **arraying** technologies such as photolithography, micro-spotting and ink jetting, coupled with sophisticated fluorescence detection systems and **bioinformatics**, permit mol. data gathering at an unprecedented rate. **Microarray**-based characterization of plant **genomes** has the potential to revolutionize plant breeding and agricultural biotechnol. This review provides an overview of DNA chip technol., focusing on manufg. approaches and biol. applications.

RETABLE

Referenced Author (RAU)	Year (RPY)	VOL (RVL)	PG (RPG)	Referenced Work (RWK)	Referenced File
Ananiev, E	1997	94	3524	Proc Natl Acad Sci U	HCAPLUS
Augenlicht, L	1991			US 4981783	HCAPLUS
Azpiroz-Leehan, R	1997	13	152	Trends Genet	HCAPLUS
Bains, W	1988	135	303	J Theor Biol	HCAPLUS
Bartel, P	1996	12	72	Nat Genet	HCAPLUS
Blanchard, A	1998			Genetic Engineering	
Chee, M	1996	274	610	Science	HCAPLUS
Cronin, M	1996	7	244	Human Mutation	HCAPLUS
de Saizieu, A	1988	16	45	Nature Biotech	
Derisi, J	1996	14	457	Nat Genet	HCAPLUS
Derisi, J	1997	278	680	Science	HCAPLUS
Donson, J	1991	88	7204	Proc Natl Acad Sci U	HCAPLUS
Drmanac, R	1993			US 5202231	HCAPLUS
Drmanac, R	1987			Yugoslav Patent Appl	
Drmanac, S	1998	16	54	Nature Biotech	MEDLINE
Fields, S	1989	340	245	Nature	HCAPLUS
Fodor, S	1991	251	767	Science	HCAPLUS
Guo, Z	1994	22	5456	Nucl Acids Res	HCAPLUS
Hacia, J	1996	14	441	Nature Genet	HCAPLUS
Hardenbol, P	1997	25	3339	Nucl Acids Res	HCAPLUS
Heller, R	1997	94	2150	Proc Natl Acad Sci U	HCAPLUS
Kallioniemi, A	1992	258	818	Science	HCAPLUS
Khrapko, K	1989	256	118	Febs Letters	HCAPLUS
Khrapko, K	1991	25	581	Mol Biol	
Kozal, M	1996	2	793	Nature Med	
Lamture, J	1994	22	2121	Nucl Acids Res	HCAPLUS
Lashkari, D	1997	94	13057	Proc Natl Acad Sci U	HCAPLUS
Liu, Y	1995	8	457	Plant J	HCAPLUS
Lockhart, D	1996	14	1675	Nature Biotechnol	HCAPLUS
Maier, E	1994	35	191	J Biotechnol	HCAPLUS
Maskos, U	1992	20	1679	Nucl Acids Res	HCAPLUS
McCusker, J	1994	136	1261	Genetics	MEDLINE

Monfort, A	1995	2	255	DNA Res	HCAPLUS
Nelson, S	1993	4	11	Nature Genet	HCAPLUS
Pease, A	1994	91	5022	Proc Natl Acad Sci U	HCAPLUS
Raz, R	1991	105	151	Gene	HCAPLUS
Sanmiguel, P	1996	274	765	Science	HCAPLUS
Sapolsky, R	1996	33	445	Genomics	HCAPLUS
Schena, M	1996	18	427	BioEssays	HCAPLUS
Schena, M	1998			PCR Methods Manual i	
Schena, M	1996	93	10614	Proc Natl Acad Sci U	HCAPLUS
Schena, M	1995	270	467	Science	HCAPLUS
Schena, M	1998	16	301	Trends Biotech	HCAPLUS
Shalon, D	1996	6	639	Genome Res	HCAPLUS
Shoemaker, D	1996	14	450	Nature Genet	HCAPLUS
Southern, E	1989			GB 8900460	
Southern, E	1996	12	110	Trends Genet	HCAPLUS
Winter, G	1991	349	293	Nature	HCAPLUS
Wodicka, L	1997	15	1359	Nature Biotech	HCAPLUS
Yershov, G	1996	93	4913	Proc Natl Acad Sci U	HCAPLUS

L138 ANSWER 44 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:322650 HCAPLUS
DN 129:90971
TI Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic mycobacterium DNA **arrays**
AU **Gingeras, Thomas R.**; Ghandour, Ghassan; Wang, Eugene; Berno, Anthony; Small, Peter M.; Drobniewski, Francis; Alland, David; Desmond, Edward; Holodniy, Mark; Drenkow, Jorg
CS Affymetrix, Santa Clara, CA, 95051, USA
SO Genome Res. (1998), 8(5), 435-448
CODEN: GEREFS; ISSN: 1088-9051
PB Cold Spring Harbor Laboratory Press
DT Journal
LA English
AB **High-d.** oligonucleotide **arrays** can be used to rapidly examine large amts. of DNA sequence in a high throughput manner. An **array** designed to det. the specific nucleotide sequence of 705 bp of the rpoB gene of Mycobacterium tuberculosis accurately detected rifampin resistance assocd. with mutations of 44 clin. isolates of M. tuberculosis. The nucleotide sequence diversity in 121 Mycobacterial isolates (comprised of 10 species) was examd. by both conventional dideoxynucleotide sequencing of the rpoB and 16S genes and by anal. of the rpoB oligonucleotide **array** hybridization patterns. Species identification of each of the isolates was similar irresp. of whether 16S sequence, rpoB sequence, or the pattern of rpoB hybridization was used. However, for several species, the no. of alleles in the 16S and rpoB gene sequences provided discordant ests. of the genetic diversity within a species. In addn. to confirming the **array**'s intended utility for sequencing the region of M. tuberculosis that confers rifampin resistance, this work demonstrates that this **array** can identify the species of nontuberculosis Mycobacteria. This demonstrates the general point that DNA **microarrays** that sequence important genomic regions (such as drug resistance or pathogenicity islands) can simultaneously identify species and provide some insight into the organism's population structure.

L138 ANSWER 45 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1998:34842 HCAPLUS
DN 128:163301
TI Bacterial transcript imaging by hybridization of total RNA to oligonucleotide **arrays**
AU de Saizieu, Antoine; Certa, Ulrich; Warrington, Janet; Gray, Christopher; Keck, Wolfgang; Mous, Jan
CS Pharma Div., F. Hoffmann-La Roche Ltd., Basel, CH-4070, Switz.
SO Nat. Biotechnol. (1998), 16(1), 45-48
CODEN: NABIF9; ISSN: 1087-0156
PB Nature America

DT Journal
LA English
AB We have used **high-d.** oligonucleotide probe **arrays** (chips) for bacterial transcript imaging. We deigned a chip contg. probes representing 106 Hemophilus influenzae genes and 100 Streptococcus pneumoniae genes. The apparent lack of polyadenylated transcripts excludes enrichment of mRNA by affinity purifn. and we thus used total, chem. biotinylated RNA as hybridization probes. We show that hybridization of Streptococcus RNA to a chip allows simultaneous quantification of the transcript levels. The sensitivity was found to be in the range of one to five transcripts per cell. The quant. chip results were in good agreement with conventional Northern blot anal. of selected genes. This technol. allow simultaneous and quant. measurement of the transcriptional activity of entire bacterial **genomes** on a single oligonucleotide probe **array.**

L138 ANSWER 46 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:804523 HCAPLUS
DN 128:98235
TI Matrix-based comparative **genomic** hybridization: **biochips** to screen for **genomic** imbalances
AU Solinas-Toldo, Sabina; Lampel, Stefan; Stilgenbauer, Stephan; Nickolenko, Jeremy; Benner, Axel; Dohner, Hartmut; Cremer, Thomas; Lichter, Peter
CS Organisation komplexer Genome, Deutsches Krebsforschungszentrum, Heidelburg, Germany
SO Genes, Chromosomes Cancer (1997), 20(4), 399-407
CODEN: GCCAES; ISSN: 1045-2257
PB Wiley-Liss, Inc.
DT Journal
LA English
AB Comparative **genomic** hybridization (CGH) to metaphase chromosomes has been widely used for the **genome**-wide screening of **genomic** imbalances in tumor cells. Substitution of the chromosome targets by a matrix consisting of an ordered set of defined nucleic acid target sequences would greatly enhance the resoln. and simplify the anal. procedure, both of which are prerequisites for a broad application of CGH as a diagnostic tool. However, hybridization of whole **genomic** human DNA to immobilized single-copy DNA fragments with complexities below the megabase pair level has been hampered by the low probability of specific binding because of the high probe complexity. We developed a protocol that allows CGH to chips consisting of glass slides with immobilized target DNAs **arrayed** in small spots. High-copy-no. amplifications contained in tumor cells were rapidly scored by use of target DNAs as small as a cosmid. Low-copy-no. gains and losses were identified reliably by their ratios by use of chromosome-specific DNA libraries or **genomic** fragments as small as 75 kb cloned in P1 or PAC vectors as targets, thus greatly improving the resoln. achievable chromosomal CGH. The ratios obtained for the same chromosomal imbalance by matrix CGH and by chromosomal CGH corresponded very well. The new matrix CGH protocol provides a basis for the development of automated diagnostic procedures with **biochips** designed to meet clin. needs.

L138 ANSWER 47 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:757153 HCAPLUS
DN 128:44651
TI Hybridization buffers and media improving the signal-to-noise ratio for assays on oligonucleotide **arrays**
IN Cronin, Maureen T.; Miyada, Charles Garrett; Trulson, Mark; **Gingeras, Thomas R.**; Mcgall, Glenn; Robinson, Claire; Oval, Michelle
PA Affymetrix, Inc., USA; Cronin, Maureen T.; Miyada, Charles Garrett; Trulson, Mark; Gingeras, Thomas R.; Mcgall, Glenn; Robinson, Claire; Oval, Michelle
SO PCT Int. Appl., 25 pp.
CODEN: PIXXD2
DT Patent
LA English

FAN.CNT 7

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9743450	A1	19971120	WO 1997-US8446	19970516
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6045996	A	20000404	US 1996-648709	19960516
	AU 9730090	A1	19971205	AU 1997-30090	19970516
PRAI	US 1996-648709	19960516			
	US 1993-143312	19931026			
	US 1994-284064	19940802			
	WO 1994-US12305	19941026			
	US 1995-510521	19950802			
	US 1995-544381	19951010			
	WO 1997-US8446	19970516			

AB Methods of improving the signal-to-noise ratio in nucleic acid hybridization assays on high-d. (>10,000 oligonucleotides/cm2) substrate-bound oligonucleotide arrays, such as the Affymetrix DNA Chip, using hybridization media that include an isostabilizing agent, a denaturing agent or a renaturation accelerant are described. Media for use with fluorescein-labeled probes are described.

L138 ANSWER 48 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:544330 HCAPLUS
DN 127:201011
TI Oligonucleotide probe **arrays** immobilized on chips, computer programs for hybridization pattern comparison, and species identification or polymorphism or mutation characterization
IN **Gingeras, Thomas A.**; Mack, David; Chee, Mark S.; Berno, Anthony J.; Stryer, Lubert; Ghandour, Ghassan; Wang, Ching
PA Affymetrix, Inc., USA; Gingeras, Thomas A.; Mack, David; Chee, Mark S.; Berno, Anthony J.; Stryer, Lubert; Ghandour, Ghassan; Wang, Ching
SO PCT Int. Appl., 132 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9729212	A1	19970814	WO 1997-US2102	19970207
	W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, US, US, US, UZ, VN, YU, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9721893	A1	19970828	AU 1997-21893	19970207
	EP 937159	A1	19990825	EP 1997-914759	19970207
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
	JP 2000504575	T2	20000418	JP 1997-528727	19970207
PRAI	US 1996-11339	19960208			
	US 1996-12631	19960301			
	US 1996-629031	19960408			
	US 1996-17765	19960515			
	WO 1997-US2102	19970207			

AB This invention provides oligonucleotide-based **arrays** and methods for speciating and phenotyping organisms, for example, using oligonucleotide sequences based on the Mycobacterium tuberculosis rpoB gene. The groups or species to which an organism belongs may be detd. by comparing hybridization patterns of target nucleic acid from the organism to hybridization patterns in a database. An example includes Mycobacterium tuberculosis gene rpoB anal. to identify mutations conferring resistance to rifampicin. A total of 25 M. tuberculosis

isolates were analyzed. Seven of these were rifampicin resistant and had mutations. Other than the mutations identified, there were no polymorphisms in any of the 25 isolates. Another example included hybridization patterns (fingerprints) for 7 clin. important Mycobacteria species: M. gordonae, M. chelonae, M. kansasii, M. scrofulaceum, M. avium, M. intracellulare, and M. xenopi.

L138 ANSWER 49 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:283823 HCAPLUS
DN 126:260132
TI Quantification of level of expression of hundreds to millions of genes using hybridization to high density synthetic oligonucleotide probe **arrays** immobilized on a surface
IN Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; **Gingeras, Thomas R.**; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
PA Affymax Technologies N.V., Neth.; Lockhart, David J.; Brown, Eugene L.; Wong, Gordon; Chee, Mark; Gingeras, Thomas R.; Mittmann, Michael P.; Lipshutz, Robert J.; Fodor, Stephen P. A.; Wang, Chunwei
SO PCT Int. Appl., 126 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9710365	A1	19970320	WO 1996-US14839	19960913
	W: AU, CA, JP, US				
	RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
	US 6040138	A	20000321	US 1995-529115	19950915
	CA 2232047	AA	19970320	CA 1996-2232047	19960913
	AU 9670734	A1	19970401	AU 1996-70734	19960913
	EP 853679	A1	19980722	EP 1996-931598	19960913
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE				
	JP 11512293	T2	19991026	JP 1996-512174	19960913
PRAI	US 1995-529115	19950915			
	WO 1996-US14839	19960913			

AB This invention provides methods of monitoring the expression levels of a multiplicity of genes. The methods involve hybridizing a nucleic acid sample to a high d. array of oligonucleotide probes where the high d. array contains oligonucleotide probes complementary to subsequences of target nucleic acids in the nucleic acid sample. In one embodiment, the method involves providing a pool of target nucleic acids comprising RNA transcripts of one or more target genes, or nucleic acids derived from the RNA transcripts, hybridizing said pool of nucleic acids to an array of oligonucleotide probes immobilized on surface, where the array comprising more than 100 different oligonucleotides and each different oligonucleotide is localized in a predetd. region of the surface, the d. of the different oligonucleotides is greater than about 60 different oligonucleotides per 1 cm2, and the oligonucleotide probes are complementary to the RNA transcripts or nucleic acids derived from the RNA transcripts; and quantifying the hybridized nucleic acids in the array.

L138 ANSWER 50 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1997:232700 HCAPLUS
DN 126:301437
TI Human immunodeficiency virus type 1 reverse **transcriptase** genotype and drug susceptibility changes in infected individuals receiving dideoxyinosine monotherapy for 1 to 2 years
AU Winters, Mark A.; Shafer, Robert W.; Jellinger, Robert A.; Mamtora, Gargi; **Gingeras, Thomas**; Merigan, Thomas C.
CS Center for AIDS Research, Stanford University, Stanford, CA, USA
SO Antimicrob. Agents Chemother. (1997), 41(4), 757-762
CODEN: AMACCQ; ISSN: 0066-4804
PB American Society for Microbiology
DT Journal

LA English
AB The genetic mechanisms of human immunodeficiency virus type 1 (HIV-1) resistance to dideoxyinosine (ddI) in vivo have been described based on data from primary HIV-1 isolates. To better define the spectrum of HIV-1 reverse transcriptase (RT) changes occurring during ddI therapy, we detd. the genotype and ddI susceptibility of the RT gene of HIV RNA isolated from the plasma of 23 patients who had received 1 to 2 yr (mean, 87 .+-. 16 wk) of ddI monotherapy. Population-based sequencing of plasma virus showed that 12 of 23 (52%) patients developed known ddI resistance mutations: L74V (7 patients), K65R (2 patients), L74V with M184V (3 patients), and L74V with K65R (1 patient). Five patients developed one or more known zidovudine resistance mutations (at codons 41, 67, 70, 215, and/or 219) during the study. Other amino acid substitutions were found, but only S68G and L210W occurred in more than one patient. Studies of sensitivity of ddI were performed on population-based recombinant-virus stocks generated by homologous recombination between a plasmid contg. an HXB2 clone with the RT gene deleted and RT-PCR products of the RT genes from patients' plasma RNA. The sequences of the virus stocks produced by this procedure were typically identical to the sequence of the input PCR product from plasma RNA. Both an MT-2 cell-based culture assay and a cell-free virion-assocd. RT inhibition assay showed that viruses possessing an L74V and/or M184V mutation or a K65R mutation had reduced sensitivity to ddI. Viruses without these specific mutations had no change in sensitivity to ddI. The results presented here show that the spectrum of RT mutations in a population of patients on ddI monotherapy is more complex than previously described. The development of multiple mutational patterns, including those that confer resistance to other nucleoside analogs, highlights the complexity of using the currently available nucleoside analogs for antiretroviral therapy.

L138 ANSWER 51 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1995:713926 HCAPLUS
DN 123:135082
TI **Arrays** of oligonucleotide probes immobilized on silica chips and selective nucleic acid hybridization for biochemical studies and medical diagnostics
IN Chee, Mark; Cronin, Maureen T.; Fodor, Stephen P. A.; **Gingeras, Thomas R.**; Huang, Xiaohua C.; Hubbell, Earl A.; Lipshutz, Robert J.; Lobban, Peter E.; Miyada, Charles Garrett; et al.
PA Affymax Technologies N.V., Neth.
SO PCT Int. Appl., 222 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 7

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9511995	A1	19950504	WO 1994-US12305	19941026
	W: AM, AT, AU, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GE, HU, JP, KE, KG, KP, KR, KZ, LK, LR, LT, LU, LV, MD, MG, MN, MW, NL, NO, NZ, PL, PT, RO, RU, SD, SE, SI, SK, TJ, TT, UA, US, UZ				
	RW: KE, MW, SD, SZ, AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
	AU 9481266	A1	19950522	AU 1994-81266	19941026
	EP 730663	A1	19960911	EP 1995-900441	19941026
	R: CH, DE, FR, GB, IT, LI, NL				
	JP 09507121	T2	19970722	JP 1994-512811	19941026
	US 5837832	A	19981117	US 1995-441887	19950516
	US 6027880	A	20000222	US 1995-544381	19951010
	US 6156501	A	20001205	US 1996-630427	19960403
	US 6045996	A	20000404	US 1996-648709	19960516
	US 5861242	A	19990119	US 1997-781550	19970109
PRAI	US 1993-143312	19931026			
	US 1994-284064	19940802			

PRAI US 1993-82937 19930625
WO 1994-US12305 19941026
US 1995-440742 19950510
US 1995-510521 19950802
US 1995-544381 19951010

AB The invention provides chips of immobilized oligonucleotide probes, and methods employing the chips, for comparing a ref. polynucleotide sequence of known sequence with a target sequence showing substantial similarity with the ref. sequence, but differing in the presence of e.g., mutations. Human immunodeficiency virus genes, cystic fibrosis genes, and the human mitochondrial genome exemplify uses of the methods.

L138 ANSWER 52 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1993:53552 HCAPLUS
DN 118:53552
TI Method and apparatus for rapid nucleic acid sequencing
IN Gilbert, Walter
PA USA
SO Eur. Pat. Appl., 60 pp.
CODEN: EPXXDW
DT Patent
LA English
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI EP 514927	A1	19921125	EP 1992-108687	19920522
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, MC, NL, PT, SE				
WO 9220824	A1	19921126	WO 1992-US4339	19920522
W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MG, MN, MW, NL, NO, PL, RO, RU, SD, SE, US				
RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GN, GR, IT, LU, MC, ML, MR, NL, SE, SN, TD, TG				
AU 9219990	A1	19921230	AU 1992-19990	19920522

PRAI US 1991-705510 19910524
WO 1992-US4339 19920522

AB An automated nucleic acid sequencer is provided comprising an oligomer synthesizer, a membrane unit **array**, a detector, and a central computer. The synthesizer synthesizes and labels multiple oligomers of predicted sequences, which are transported to selected membranes contained within a membrane unit **array**, where they are hybridized to sequencing patterns bound to the membranes. A detector detects the hybridized sequencing patterns and sends descriptions of those patterns to the central computer, which analyzes those descriptions to construct a nucleic acid sequence, predicts a next set of oligomers for subsequent hybridizations, and selects corresponding membranes for hybridization with each predicted oligomer. Under computer control, synthesis of multiple oligomers, hybridization within multiple membranes, detection of the resulting patterns on multiple membranes, prediction of next oligomers, and selection of corresponding membranes, proceed simultaneously in accordance with the steps of a method of automated sequencing. A method using the app. for sequencing is also provided.

L138 ANSWER 53 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1992:627229 HCAPLUS
DN 117:227229
TI Automated DNA hybridization **array** construction and database design for robotic control and for source determination of hybridization responses
AU Medvick, Patricia A.; Hollen, Robert M.; Roberts, Randy S.; Trimmer, Dave; Beugelsdijk, Tony J.
CS Cent. Hum. Genome Stud., Los Alamos Natl. Lab., Los Alamos, NM, 87545, USA
SO Int. J. Genome Res. (1992), 1(1), 17-23
CODEN: IJGREY
DT Journal
LA English
AB The human **genome** effort has highlighted a huge area for

potential automation that is necessary in order for the program to succeed. Much of the work in prepg. maps of individual human chromosomes involves labor-intensive highly repetitive tasks. The authors concd. on automating the procedure of gridding hybridization membranes from microtiter-well plates and on developing a database for robotic control and for initial storage of hybridization results. On the basis of numerous interactions with biologists on the human **genome** project, a gridding system was designed to produce **high-d.** grids on a 20- by 22-cm membrane, to require initial user interactions for setup, and, thereafter, to proceed untended with the gridding of the membrane. The software is written in the object-oriented style of the Robot Independent Programming Language (RIPL), developed by Sandia National Labs., to increase flexibility and maintainability. A path table in a relational database provides location information to the robotic arm and permits rapid changes in the robot movement patterns. Database tables track an individual microtiter well to its membrane location. Planned system improvements include incorporating a UNIX-based computer workstation with object-oriented database for integrating the initial colony-picking, membrane gridding and hybridized membrane film assessment into one system.

L138 ANSWER 54 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1992:606336 HCAPLUS
DN 117:206336
TI **Transcription**-based nucleic acid amplification system by two-enzyme, self-sustained sequence replication
IN Fahy, Eoin David; Kwoh, Deborah Yantis; **Gingeras, Thomas Raymond**; Guatelli, John Christopher; Whitfield, Kristina Marie
PA Siska Diagnostics, Inc., USA
SO PCT Int. Appl., 95 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 9208800	A1	19920529	WO 1991-US8488	19911113
	W: AT, AU, BB, BG, BR, CA, CH, CS, DE, DK, ES, FI, GB, HU, JP, KP, KR, LK, LU, MC, MG, MN, MW, NL, NO, PL, RO, SD, SE, SU				
	RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, DE, DK, ES, FR, GA, GB, GN, GR, IT, LU, ML, MR, NL, SE, SN, TD, TG				
	ZA 9108965	A	19920826	ZA 1991-8965	19911112
	IL 100040	A1	19951231	IL 1991-100040	19911112
	CA 2096013	AA	19920514	CA 1991-2096013	19911113
	AU 9191315	A1	19920611	AU 1991-91315	19911113
	EP 572417	A1	19931208	EP 1992-901557	19911113
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE				
	JP 06502767	T2	19940331	JP 1992-502286	19911113
	HU 69772	A2	19950928	HU 1993-1369	19911113
	NO 9301709	A	19930712	NO 1993-1709	19930511
PRAI	US 1990-612688	19901113			
	WO 1991-US8488	19911113			

OS MARPAT 117:206336
AB A transcription-based nucleic acid amplification system (TAS) uses RNA-dependent DNA polymerase, DNA-dependent DNA polymerase, RNase H, and DNA-dependent RNA polymerase activities for detecting a target RNA is described. The method transcribes an RNA to cDNA that is converted to the double-stranded form that is then transcribed to give an RNA for another round of conversion to the cDNA. The system also requires primers that contain a promoter sense sequence and does not require thermal denaturation between each round of amplifications. RNase H, e.g. from Escherichia coli, may be added to improve efficiency. The system is optimized by addn. to the reaction medium of >1 of C1-10 alc., a sugar alc., a polyethylene glycol, a sugar, and a sulfoxide. Detection of the cystic fibrosis-assocd. gene is demonstrated. The RNA was amplified using reverse transcriptase (avian myeloblastosis virus) for 1 min, then

incubated with reverse transcriptase, T7 RNA polymerase, and RNAase H. The amplified nucleic acid was detected by binding to immobilized oligonucleotides.

L138 ANSWER 55 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1992:167323 HCAPLUS
DN 116:167323
TI Development of an automated workcell for DNA hybridization **array** construction
AU Medvick, Patricia A.; Hollen, Robert M.; Roberts, Randy S.
CS Rob. Sect., Los Alamos Natl. Lab., Los Alamos, NM, 87545, USA
SO Lab. Rob. Autom. (1991), 3(4-5), 169-73
CODEN: LRAUEY; ISSN: 0895-7533
DT Journal
LA English
AB The human **genome** effort has highlighted a huge area for potential automation. Much of the work involved in prepg. maps of individual human chromosomes involves highly repetitive procedures. Efforts in technol. development have been directed toward gridding hybridization membranes from microtiter-well plates, data base development for robotic control, and initial storage of hybridization results. On the basis of requirements for **high-d.** grids, the authors designed a current automated gridding system with a 30-plate dispenser and a restacker to permit unattended performance. The hardware includes a NUTEC gantry robot with a Motion Science controller, a Zymark microtiterplate dispenser, a restacker, a Keithley control system, a Symbol Technologies bar code reader, a metal-pinned gridding tool, a sterilization station, a plate-lid holder, and an IBM personal computer. The software, originally written in C, has been converted to C + + in the object-oriented style of the Robot Independent Programming Language (RIPL) developed by Sandia National Labs. to increase maintainability. A relational data base provides location information to the robotic arm. A path table permits rapid changes in the robot movement patterns. The data base tables make it possible to track an individual microtiter well through the gridding and subsequent radioactive-probe test. We can now stack 30 trays at a time for unattended gridding onto one or two membranes of one to six sectors with an interleave d. of 1, 4, 9, or 16 dots per well location. Arbitrary interleaves are also possible. Planned system improvements include incorporating a UNIX-based computer workstation for integrating the initial colony picking, membrane gridding, and hybridized membrane film assessment. Information gathered will be stored in an object-oriented data base for perusal prior to entry into the Los Alamos Lab. Notebook and the **genome** data base.

L138 ANSWER 56 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1991:671659 HCAPLUS
DN 115:271659
TI Self-sustained sequence replication (3SR): an isothermal **transcription**-based amplification system alternative to PCR
AU Fahy, E.; Kwoh, D. Y.; **Gingeras, T. R.**
CS Salk Inst. Biotechnol./Ind. Assoc., San Diego, CA, 92186, USA
SO PCR Methods Appl. (1991), 1(1), 25-33
CODEN: PMAPES; ISSN: 1054-9803
DT Journal; General Review
LA English
AB A review with 47 refs. on the method of self-sustained sequence replication (3SR), optimization of the 3SR reaction, and its reaction conditions (oligonucleotide primers, nucleotide triphosphates, monovalent cations, and enzymes).

L138 ANSWER 57 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1991:509515 HCAPLUS
DN 115:109515
TI **Methodologies** for in vitro nucleic acid amplification and their applications
AU **Gingeras, T. R.**; Richman, D. D.; Kwoh, D. Y.; Guatelli, J. C.

CS Salk Inst. Biotechnol., Ind. Assoc., Inc., La Jolla, CA, 92037, USA
SO Vet. Microbiol. (1990), 24(3-4), 235-51
CODEN: VMICDQ; ISSN: 0378-1135
DT Journal; General Review
LA English
AB A review with 30 refs. The capability to detect the genetic elements (DNA or RNA) of a particular pathogen as a means of identifying the infectious agent has been the traditional function of nucleic acid hybridization assays. The low copy no. of genetic material from several types of viral pathogens fostered the development of in vitro nucleic acid amplification methods as a means to increase the copy no. of the characteristic genetic elements of pathogenic agents. The polymerase chain reaction (PCR) and a transcription-based amplification system (TAS) are 2 amplification methods that have been developed to serve this function. Both methods were employed to study both genetic and infectious disease problems. The characteristics of these amplification methods are discussed, and some of their applications, esp. in the study of HIV-1, are described.

L138 ANSWER 58 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1990:193187 HCAPLUS
DN 112:193187
TI A **transcription**-based amplification system
AU **Gingeras, Thomas R.**; Davis, G. R.; Whitfield, K. M.; Chappelle, H. L.; DiMichele, L. J.; Kwoh, D. Y.
CS Salk Inst. Biotechnol. Ind. Assoc., Inc., San Diego, CA, 92138, USA
SO PCR Protoc.: Guide Methods Appl. (1990), 245-52. Editor(s): Innis, Michael A. Publisher: Academic, San Diego, Calif.
CODEN: 56TMAY
DT Conference
LA English
AB An RNA transcription-based amplification system (TAS) is described. Enhancements of the polymerase chain reaction (PCR) protocol have been described and include the addn. of the phage T7 RNA polymerase recognition sequences to PCR primers such that after multiple cycles of PCR, RNA transcripts can be produced from the PCR-amplified DNA. Each cycle of TAS copies a segment (100 to 500 bases) of an RNA or DNA target mol. into 20 to 100 copies of RNA. A single cycle of TAS is composed of a cDNA step (to convert a target nucleic acid sequence to a cDNA template contg. an RNA polymerase-binding site) and an RNA transcription step (to increase the copy no. of the cDNA template). Consequently, relatively few cycles are required to achieve high levels of sequence-specific amplifications (105- to 106-fold increases). The specificity of the TAS protocol can be enhanced by the use of a bead-based sandwich hybridization system (BBSHS). This sandwich hybridization approach fits well with the single-stranded nature of the TAS products and permits direct anal. of the results of the TAS reaction. A protocol is presented for the application of TAS to the detection of HIV-1 in culture lymphocytes.

L138 ANSWER 59 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1989:491722 HCAPLUS
DN 111:91722
TI **Transcription**-based nucleic acid amplification/detection systems
IN **Gingeras, Thomas Raymond**; Merten, Ulrich; Kwoh, Deborah Yantis
PA Siska Diagnostics, Inc., USA
SO PCT Int. Appl., 86 pp.
CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 8810315	A1	19881229	WO 1988-US2108	19880617
	W: AU, BR, DK, FI, HU, JP, KR, NO, SU				
	RW: AT, BE, CH, DE, FR, GB, IT, LU, NL, SE				
	IL 86724	A1	19950124	IL 1988-86724	19880613
	AU 8821265	A1	19890119	AU 1988-21265	19880617

	AU 623602	B2	19920521		
	ZA 8804350	A	19890329	ZA 1988-4350	19880617
	ES 2009286	A6	19890916	ES 1988-1899	19880617
	BR 8807097	A	19891017	BR 1988-7097	19880617
	JP 02500565	T2	19900301	JP 1988-506404	19880617
	JP 2843586	B2	19990106		
	EP 368906	A1	19900523	EP 1988-906601	19880617
	EP 368906	B1	19941123		
	EP 368906	B2	19990804		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	HU 52823	A2	19900828	HU 1988-4791	19880617
	HU 216317	B	19990628		
	EP 623683	A1	19941109	EP 1994-200266	19880617
	EP 623683	B1	20000927		
	R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE				
	AT 196657	E	20001015	AT 1994-200266	19880617
	NO 8905090	A	19900219	NO 1989-5090	19891218
	DK 8906444	A	19900219	DK 1989-6444	19891219
	FI 93743	B	19950215	FI 1989-6077	19891219
	FI 93743	C	19950526		

PRAI US 1987-64141 19870619
US 1988-202978 19880606
EP 1988-906601 19880617
WO 1988-US2108 19880617

AB A method for amplification and detection of a nucleic acid comprising prodn. of an RNA transcript, and optionally, reverse transcription of this RNA transcript followed by another round of amplification is described. The basic process comprises 2 steps. First, prodn. of a double-stranded DNA (dsDNA) from the target DNA or RNA such that the dsDNA contains an RNA polymerase promoter. This is done through the use of a primer which contains the promoter and is addnl. complementary to a portion of the target nucleic acid; prepn. of cDNA contg. this primer; hybridization of a 2nd primer to this cDNA; and prepn. of dsDNA from this 2nd primer. Second, in an amplification step, the dsDNA is transcribed with a bacteriophage RNA polymerase. An optional second amplification step comprises formation of DNA complementary to this RNA transcript through use of reverse transcriptase followed by a repetition of the described process. The target nucleic acid may be assocd. with a genetic or pathogenic disease, e.g. it may be a virus. The method was used to detect HIV in human blood samples.

L138 ANSWER 60 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1989:167494 HCAPLUS
DN 110:167494
TI **Transcription**-based amplification system and detection of amplified human immunodeficiency virus type 1 with a bead-based sandwich hybridization format
AU Kwoh, D. Y.; Davis, G. R.; Whitfield, K. M.; Chappelle, H. L.; DiMichele, L. J.; **Gingeras, T. R.**
CS SISKA Diagn., La Jolla, CA, 92037, USA
SO Proc. Natl. Acad. Sci. U. S. A. (1989), 86(4), 1173-7
CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB The in vitro amplification of biol. important nucleic acid has proceeded principally by a strategy of DNA replication. Polymerase chain reaction was the first such protocol to achieve this goal. In this report, a transcription-based amplification system (TAS) is described. Each cycle of the TAS is composed of two steps. The first is a cDNA synthesis step that produces one copy of a double-stranded DNA template for each copy of RNA or DNA target nucleic acid. During the course of this cDNA synthesis step, a sequence recognized by a DNA-dependent RNA polymerase is inserted into the cDNA copy of the target sequence to be amplified. The second step is the amplification of the target sequence by the transcription of the cDNA template into multiple copies of RNA. This procedure has been applied to the detection of human immunodeficiency virus type 1

(HIV-1)-infected cells. After four cycles of TAS, the amplification of the vif region of the HIV-1 RNA genome was measured to be, on the av., 38-47-fold per cycle, resulting in a 2-5 .times. 106-fold increase in the copy no. of the original target sequence. This amplification by the TAS protocol allows the detection of fewer than one HIV-1-infected CEM cell in a population of 106 uninfected CEM cells. Detection of the TAS-generated RNA from HIV-1-infected cells can easily be accomplished by means of a bead-based sandwich hybridization protocol, which provides addnl. specificity for the identification of the amplified HIV-1-specific sequence.

L138 ANSWER 61 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1983:534554 HCAPLUS
DN 99:134554
TI Information content of the adenovirus-2 **genome**
AU Roberts, R. J.; Sciaky, D.; Gelinas, R. E.; Jiang, B. D.; Yen, C. E.; Kelly, M. M.; Bullock, P. A.; Parsons, B. L.; O'Neill, K. E.; **Gingeras, T. R.**
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO Cold Spring Harbor Symp. Quant. Biol. (1983), Volume Date 1982, 47(2), 1025-37
CODEN: CSHSAZ; ISSN: 0091-7451
DT Journal
LA English
AB A discussion is given on the information content of the adenovirus 2 (Ad2) genome, stressing the early regions 1, 2B, and 4 and those regions coding for the IVa2 and 52,55 kilodalton polypeptides. Coding information is used very economically in the Ad2 genome. Intergene distances are short, and there are several overlapping genes.

L138 ANSWER 62 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1982:609475 HCAPLUS
DN 97:209475
TI Nucleotide sequences from the adenovirus-2 **genome**
AU **Gingeras, Thomas R.**; Sciaky, Daniela; Gelinas, Richard E.; Jiang, Bing Dong; Yen, Clifford E.; Kelly, Margaret M.; Bullock, Peter A.; Parsons, Barbara L.; Neill, Kathy E.; Roberts, Richard J.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO J. Biol. Chem. (1982), 257(22), 13475-91
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The sequence of 15,441 nucleotides from the adenovirus-2 genome was detd. and includes the regions between coordinates 0-32% and 89-100%. These regions contain the early (E) transcription units E1A, E1B, E2B, and E4, the genes for polypeptides IVa2 and IX, the CO2H terminus of fiber polypeptide, as well as the 2 VA RNAs and the leader sequences for the major late mRNAs. Anal. of tryptic peptides from the terminal protein and its precursor allowed the gene for the precursor terminal protein to be positioned between coordinates 28.9 and 23.5 on the l-strand. A min. mol. wt. of 74,500 is predicted. A 2nd, longer open reading frame is also found on the l-strand between coordinates 22.9 and 14.2 and predicts a polypeptide of mol. wt. .gtoreq.120,000. Many open reading frames corresponding to peptide mol. wt. >10,000 exist within this sequence, although <50% of them can be assigned to previously characterized polypeptides. As with other viral genomes, the available coding information is highly compressed. Intergenic distances are very short and examples are found of genes which overlap on either the same strand or the complementary strand.

L138 ANSWER 63 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1982:98768 HCAPLUS
DN 96:98768
TI A semiautomated method for the reading of nucleic acid sequencing gels
AU **Gingeras, Thomas R.**; Rice, P.; Roberts, R. J.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA

SO Nucleic Acids Res. (1982), 10(1), 103-14
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A collection of computer programs is described which permit automatic entering of nucleotide sequence data directly from an electrophoresis gel autoradiograph into a computer. This collection, called DIGITPAD, makes use of a digitizing tablet for the data entry and allows the rapid and accurate transfer of the sequence into the computer.

L138 ANSWER 64 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1981:493117 HCAPLUS
DN 95:93117
TI Computer assisted methods for nucleic acid sequencing
AU **Gingeras, T. R.**; Roberts, R. J.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO Genet. Eng. (1981), 3, 319-38
CODEN: GENGDC; ISSN: 0196-3716
DT Journal; General Review
LA English
AB A review with 45 refs.

L138 ANSWER 65 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1980:600224 HCAPLUS
DN 93:200224
TI Steps toward computer analysis of nucleotide sequences
AU **Gingeras, Thomas R.**; Roberts, Richard J.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO Science (Washington, D. C.) (1980), 209(4463), 1322-8
CODEN: SCIEAS; ISSN: 0036-8075
DT Journal; General Review
LA English
AB A review with 40 refs. Advances in recombinant DNA technol. have allowed the isolation of large nos. of biol. interesting fragments of DNA. Concomitant improvements in methods for nucleic acid sequencing have led many investigators to characterize their clones by sequencing them. This has resulted in the accumulation of such large amts. of sequence data that computer-assisted methods, with programs directed toward the manipulation of nucleic acid sequences, have become indispensable during the collection and anal. of that data.

L138 ANSWER 66 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1979:606877 HCAPLUS
DN 91:206877
TI Computer programs for the assembly of DNA sequences
AU **Gingeras, T. R.**; Milazzo, J. P.; Sciaky, D.; Roberts, R. J.
CS Cold Spring Harbor Lab., Cold Spring Harbor, NY, 11724, USA
SO Nucleic Acids Res. (1979), 7(2), 529-45
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A collection is described of user-interactive computer programs which aid in the assembly of DNA sequences. This is achieved by searching for the positions of overlapping common nucleotide sequences within the blocks of sequence obtained as primary data. Such overlapping segments are then melded into 1 continuous string of nucleotides. Strategies for detg. the accuracy of the sequence being analyzed and reducing the error rate resulting from the manual manipulation of sequence data are discussed. Sequences mapping from 97.3 to 100% of the adenovirus 2 genome were used to demonstrate the performance of these programs.

L138 ANSWER 67 OF 67 HCAPLUS COPYRIGHT 2001 ACS
AN 1979:50495 HCAPLUS
DN 90:50495
TI A computer assisted method for the determination of restriction enzyme recognition sites

AU **Gingeras, T. R.**; Milazzo, J. P.; Roberts, R. J.
CS Cold Spring Harbor Lab., Cold Spring Habor, N. Y., USA
SO Nucleic Acids Res. (1978), 5(11), 4105-27
CODEN: NARHAD; ISSN: 0305-1048
DT Journal
LA English
AB A computer program was developed which aids in the detn. of restriction enzyme recognition sequences. This was achieved by cleaving DNAs of known sequence with a restriction endonuclease and comparing the fragmentation pattern with a computer-generated set of patterns. The feasibility of this approach was tested using fragmentation patterns of phage .phi.X174 DNA produced by enzymes of both known and unknown specificity. Recognition sequences were predicted for 2 restriction endonucleases (BbvI and SfaNI) using this method. In addn., recognition sequences were predicted for 2 other enzymes (PvuI and MstI) using another computer-assisted method.

=> dh is

DH IS NOT A RECOGNIZED COMMAND
The previous command name entered was not recognized by the system.
For a list of commands available to you in the current file, enter
"HELP COMMANDS" at an arrow prompt (=>).

=> d his

(FILE 'HOME' ENTERED AT 11:56:22 ON 26 JAN 2001)
SET COST OFF

FILE 'BIOSIS' ENTERED AT 11:56:43 ON 26 JAN 2001
E ROSENOW C/AU
L1 17 S E3,E4,E6
E GINGERASE T/AU
E GINGERAS T/AU
L2 69 S E3-E7
L3 85 S L1,L2
L4 1 S L3 AND 00530/CC
L5 2 S L3 AND 04500/CC
L6 56 S L3 AND (0350# OR 10052 OR 10062)/CC
L7 17 S L3 AND GENOM?
L8 28 S L3 AND TRANSCRI?
L9 13 S L3 AND HYBRID?
L10 4 S L3 AND OPERON
L11 0 S L3 AND PROKARY?
L12 12 S L3 AND (ESCHER? OR "E")()COLI
L13 12 S L3 AND ENTEROBACTERIACEAE+NT/BC
L14 69 S L3 AND (GENE OR GENETIC? OR DNA OR CDAN OR NUCLEIC ACID OR OL
L15 79 S L6-L14
L16 1 S L15 AND L4
L17 3 S L14 AND (SOFTWARE OR SOFT WARE OR COMPUTER? OR PROGRAM(S)CODE
L18 6 S L14 AND (GENECHIP? OR BIOCHIP? OR MICROCHIP? OR CHIP)
L19 8 S L4,L5,L16-L18
L20 13 S L15 AND HYBRID?
L21 2 S L20 AND L19
L22 8 S L19,L21
L23 11 S L20 NOT L22
L24 18 S L15 AND ?ARRAY?
L25 9 S L24 AND L16-L23
L26 11 S L22,L25
L27 17 S L23,L24 NOT L26
L28 13 S L26-L27 AND DENSITY
L29 18 S L26-L27 AND ?ARRAY?
L30 18 S L28,L29
L31 8 S L27,L27 NOT L30

```
L32           1 S L31 AND SOLID SUPPORT CHEMISTRIES/TI
L33          19 S L30,L32

     FILE 'BIOSIS' ENTERED AT 12:10:48 ON 26 JAN 2001
L34          59 S  GENECHIP
L35          55 S L34 NOT L33
L36          15 S L35 AND AFFYMETRIX
L37          10 S L35 AND AFFYMETRIX/CS
L38          24 S L36,L37
L39          31 S L34 NOT L33,L38
L40          13 S L39 AND GENECHIP/TI
L41          18 S L39 NOT L40
L42          31 S L39-L41
L43          17 S L42 AND ?ARRAY?
L44           7 S L42 AND DENSITY
L45          12 S L42 AND (MUTANT? OR MUTAT? OR MISMATCH? OR DELETION OR TRANSC
L46          22 S L43-L45
L47           9 S L42 NOT L46
L48          31 S L42-L47
L49           3 S L48 AND (SOFTWARE OR DATABASE OR DATA BASE OR COMPUTER? OR PR
L50          31 S L48,L49

     FILE 'MEDLINE' ENTERED AT 12:23:07 ON 26 JAN 2001
                 E ROSENOW C/AU
L51           9 S E3
                 E GINGERAS T/AU
L52          45 S E3,E4
L53          54 S L51,L52
L54          12 S GENECHIP
                 E SEQUENCE ANALYSIS/CT
L55       38171 S E3+NT/CT
L56       31864 S E5+NT/CT
                 E OLIGONUCLEOTIDE ARRAY SEQUENCE/CT
L57         351 S E4+NT/CT
                 E E12+ALL/CT
L58       38171 S L55-L57
L59           8 S L58 AND L53
L60           8 S L58 AND L54
L61          16 S L59,L60
L62           4 S L54 NOT L61
L63           2 S L62 AND (GENECHIP? OR HIGH DENSITY)/TI
L64          18 S L61,L63
L65          46 S L53 NOT L64
                 SEL DN 26 38 40 43 46
L66           5 S  E1-E5
L67          23 S L64,L66
                 E HYBRIDIZATION/CT
                 E E3+ALL/CT
L68        7003 S  E7+NT/CT
                 E NUCLEIC ACID HYBRIDIZATION/CT
                 E E3+ALL/CT
L69       69977 S E7+NT/CT
                 E TRANSCRIPT/CT
                 E E9+ALL/CT
                 E E2+ALL/CT
L70      150468 S E11+NT/CT
L71       14796 S L68,L69 AND L70
                 E GENOME/CT
                 E E3+ALL/CT
L72       18380 S E6+NT/CT
L73         227 S L72 AND L71
L74         192 S L73 AND ?SEQUENC?
L75           2 S L73 AND SOFTWARE
                 E SOFTWARE/CT
                 E E3+ALL/CT
L76      312381 S E4+NT/CT
```

```
L77        340113 S E3+NT/CT
L78            15 S L76,L77 AND L73
L79            14 S L74 AND L78
L80            15 S L75,L78,L79
L81            11 S L80 AND ?ARRAY?
L82             4 S L80 NOT L81
L83             3 S L82 NOT DROSOPH?
L84            14 S L81,L83
L85            37 S L67,L84

     FILE 'MEDLINE' ENTERED AT 12:39:19 ON 26 JAN 2001

     FILE 'HCAPLUS' ENTERED AT 12:42:54 ON 26 JAN 2001
                 E GENECHIP
L86            45 S E3-E5
L87            67 S GENE CHIP
L88           111 S L86,L87
L89           484 S BIOCHIP OR BIO CHIP
L90          1201 S BIOINFORMATIC
L91          1769 S L86-L90
                 E SOFTWARE/CT
                 E E3_ALL/CT
                 E SOFTWARE/CT
                 E E3+ALL/CT
L92         44466 S E2+NT/CT
L93          2302 S COMPUTER APPLICATIONS+NT/CT
                 E COMPUTER APPLICAITON/CT
                 E COMPUTER APPLICATION/CT
L94         30881 S E3+NT/CT
                 E COMPUTER/CT
                 E E3+ALL/CT
L95          3580 S E2+NT/CT
                 E E2+ALL//CT
                 E E3+ALL/CT
L96         47727 S E3+NT OR E11+NT/CT
L97         78030 S L91-L96
L98          5293 S L97 AND ?SEQUENC?
L99          1178 S L97 AND GENOM?
L100            1 S L93 AND L99
L101        19436 S HIGH DENSITY
L102          314 S L101 AND ?ARRAY?
L103           20 S L102 AND L97
L104           28 S L102 AND GENOM?
L105           51 S L102 AND SEQUENC?
L106           70 S L103-L105
L107           52 S L106 AND HYBRID?
L108           13 S L107 AND TRANSCRI?

     FILE 'HCAPLUS' ENTERED AT 12:51:53 ON 26 JAN 2001
L109           39 S L107 NOT L108
L110         1437 S PROKARYO? AND GENOM?
L111          360 S L110 AND TRANSCRI?
L112           45 S L111 AND OPERON
L113           57 S L111 AND HYBRID?
L114            5 S L112 AND L113
L115           51 S L113 NOT L108,L109,L114
L116        15145 S NUCLEIC ACID HYBRIDIZATION+NT/CT
                 E NUCLEIC ACID HYBRIDIZATION/CT
                 E E3+ALL/CT
L117           15 S E3+NT/CT
L118        15145 S E2+NT/CT
L119         2736 S L116-L118 AND GENOM?
                 E GENOME/CT
                 E E3+ALL/CT
L120         1525 S L116-L118 AND (E2 OR E3 OR E4+NT/CT OR E6+NT/CT)
L121         3519 S L119,L120
```

```
L122        63 S L121 AND HIGH()(D OR DENSITY OR INTENS?)
L123       201 S L121 AND ?ARRAY?
L124       225 S L122,L123
L125        38 S L124 AND L97
L126        36 S L125 NOT L108,L109
               E ROSENOW C/AU
L127        11 S E4,E5
               E GINGERAS T/AU
L128        73 S E4-E8
L129        84 S L127,L128
L130        12 S L129 AND L97
L131        16 S L129 AND ?ARRAY?
L132        12 S L129 AND HIGH()(D OR DENSITY OR INTENS?)
L133         0 S L129 AND PLURAL?
L134        17 S L130-L132 NOT L108,L109
L135        53 S L126,L134
L136        67 S L129 NOT L135
L137        14 S L136 AND (METHODOLOG? OR ARRAY? OR GENOME OR TRANSCRIP?)/TI
L138        67 S L135,L137
               SET COST ON
```